



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 180248

TO: Sean McGarry
Art Unit: 1635
Location: REM/2D19/2C19
Serial Number: 10/655801

Friday, March 03, 2006

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Published Applications Database - November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New).

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STIC-Biotech/ChemLib

180248

44
ARF

From: McGarry, Sean
Sent: Wednesday, February 22, 2006 3:13 PM
To: STIC-Biotech/ChemLib
Subject: SEQ SEARCH 10/655,801

Sean McGarry
AU 1635
REM 02D19 Office
REM 2C18 Mailbox
X20761
73484

10/655,801

Please, a length limited search of SEQ ID NOS: 19-22 and nucleotides 14-177 of SEQ ID NO: 3 (nt \leq 80).

Thank You.

mg
19 na 18
20 18
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22 18
3 na 4145

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
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Date completed: _____
Searcher: Beverly e 2528
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Search Site
____ STIC
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Type of Search
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Vendors
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: March 3, 2006, 07:16:16 ; Search time 3434.27 Seconds
(without alignments)
2714.499 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5881141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2389942

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_in.*
- 3: gb_env.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sta.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vi.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	16.5	75	6	AX391505 Sequence
2	27	16.5	75	6	AX391607 Sequence
3	25.4	15.5	75	6	AX391506 Sequence
4	25.4	15.5	75	6	AX391608 Sequence
5	23.6	14.4	65	6	CQ556308 Sequence
6	22	13.4	65	6	CQ534115 Sequence
7	21.8	13.3	78	6	AR101987 Sequence
8	21.8	13.3	78	6	BD064232 Therapy f
9	21.8	13.3	78	6	CS105031 Sequence
10	21.8	13.3	78	6	AR322465 Sequence
11	21.8	13.3	78	6	AR372141 Sequence
12	21.8	13.3	78	8	HUNGHPA
13	21.8	13.3	80	6	I00999 Human precu
14	21.8	13.3	80	6	I02190 Sequence 2
15	21.4	13.0	65	6	CQ554646 Sequence
16	21.2	12.9	65	6	CQ530857 Sequence
17	21	12.8	75	11	CS001411 Sequence
18	20.6	12.6	50	6	CS063833 Sequence

C 92 18.4 11.2 45 6 CQ892571 Sequence
 93 18.4 11.2 47 6 AR288279 Sequence
 C 94 18.4 11.2 51 6 CQ003842 Sequence
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 96 18.4 11.2 51 6 AX157558 Sequence
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 98 18.4 11.2 51 8 AF079053 Homo sapi
 99 18.4 11.2 60 6 CQ535939 Sequence
 100 18.4 11.2 60 6 CQ537391 Sequence

ALIGNMENTS

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 ACCESSION AX391505
 VERSION AX391505.1 GI:19700113
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Adamczewski, M., Ebbinghaus-Kintscher, U., Methfessel, C. and Schulte, T.
 TITLE Acetylcholine receptor subunits
 JOURNAL Patent: EP 1184391-A 16 06-MAR-2002;
 BAYER AG (DE)
 FEATURES Location/Qualifiers
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 /mol_type="unassigned DNA"
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 /note="Primer"

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 QY 78 TTGACTGTCTCTTACC 92
 DB 61 GCGACGAGCCCTACC 75

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 LOCUS AX391607 75 bp DNA linear PAT 23-MAR-2002
 DEFINITION Sequence 20 from Patent EP1184390.
 ACCESSION AX391607
 VERSION AX391607.1 GI:19700213
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Adamczewski, M., Ebbinghaus-Kintscher, U., Methfessel, C. and Schulte, T.
 TITLE Acetylcholine receptor subunits
 JOURNAL Patent: EP 1184390-A 20 06-MAR-2002;
 BAYER AG (DE)
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 DEFINITION Sequence 17 from Patent EP1184391.
 ACCESSION AX391506
 VERSION AX391506.1 GI:19700114
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Adamczewski, M., Ebbinghaus-Kintscher, U., Methfessel, C. and Schulte, T.
 TITLE Acetylcholine receptor subunits
 JOURNAL Patent: EP 1184391-A 17 06-MAR-2002;
 BAYER AG (DE)
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 QY 78 TTGACTGTCTCTTACC 92
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 LOCUS AX391608 75 bp DNA linear PAT 23-MAR-2002
 DEFINITION Sequence 21 from Patent EP1184390.
 ACCESSION AX391608
 VERSION AX391608.1 GI:19700214
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Adamczewski, M., Ebbinghaus-Kintscher, U., Methfessel, C. and Schulte, T.
 TITLE Acetylcholine receptor subunits
 JOURNAL Patent: EP 1184390-A 21 06-MAR-2002;
 BAYER AG (DE)
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RESULT 5
CQ556308 65 bp DNA linear PAT 30-JAN-2004
LOCUS
DEFINITION Sequence 25943 from Patent WO0210449.
ACCESSION CQ556308
VERSION CQ556308.1 GI:41522735
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
JOURNAL variants that populate a transcriptome
Patent: WO 0210449-A 25943 07-FEB-2002;
CompuGen Inc. (US)
FEATURES
Location/Qualifiers
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DEFINITION Sequence 3750 from Patent WO0210449.
ACCESSION CQ534115
VERSION CQ534115.1 GI:41500379
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
REFERENCE 1
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
JOURNAL variants that populate a transcriptome
Patent: WO 0210449-A 3750 07-FEB-2002;
CompuGen Inc. (US)
FEATURES
Location/Qualifiers
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QY 35 CTAGACAGTCCCGAAGTCTCAAGGCACAGGTCTCTTCTGCTTTGACTGCTTACCCC 94
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QY 95 GGGGAGGAGGAGTGC 107
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RESULT 7
BD064232 78 bp DNA linear PAT 14-FEB-2001
LOCUS
DEFINITION Therapy for alpha-galactosidase A deficiency.
ACCESSION BD064232
VERSION BD064232.1 GI:22609835
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 78)
AUTHORS Seiden,R.F., Borowski,M., Gillespie,F.P., Kinoshita,C.M.,
TITLE Treco,D.A. and Williams,M.D.
JOURNAL Therapy for alpha-galactosidase A deficiency
Patent: JP 2001504324-A 21 '03-APR-2001;
TRANSMARKYOTIC THERAPIES INC
COMMENT PN JP 2001504324-A/21
PD 03-APR-2001
PF 12-SEP-1997 JP 1998514004

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QY 77 TT 78
Db 4 GT 3

RESULT 7
ARI01987 78 bp DNA linear PAT 14-FEB-2001
LOCUS
DEFINITION Sequence 22 from patent US 6083725.
ACCESSION ARI01987
VERSION ARI01987.1 GI:12812785
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 78)
AUTHORS Selden,R.F., Borowski,M., Gillespie,F.P., Kinoshita,C.M.,
TITLE Treco,D.A. and Williams,M.D.
JOURNAL Transfected human cells expressing human .alpha.-galactosidase A
protein
Patent: US 6083725-A 22 04-JUL-2000;
CompuGen Inc. (US)
FEATURES
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RESULT 8
BD064232 78 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Therapy for alpha-galactosidase A deficiency.
ACCESSION BD064232
VERSION BD064232.1 GI:22609835
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 78)
AUTHORS Seiden,R.F., Borowski,M., Gillespie,F.P., Kinoshita,C.M.,
TITLE Treco,D.A. and Williams,M.D.
JOURNAL Therapy for alpha-galactosidase A deficiency
Patent: JP 2001504324-A 21 '03-APR-2001;
TRANSMARKYOTIC THERAPIES INC
COMMENT PN JP 2001504324-A/21
PD 03-APR-2001
PF 12-SEP-1997 JP 1998514004

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PR 13-SEP-1996 US 08/712614
PI RICHARD F SELDEN, MARIANNE BOROWSKI, FRANCES
P GILLESPIE, CAROL M
PI KINOSHITA,
PI DOUGLAS A TRECO, MELANIE D WILLIAMS
PC C12N9/40, C12N15/62, C12N15/56, A61K38/47, A61K48/00, C12N5/10 CC
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LOCUS
DEFINITION Sequence 22 from Patent EP1538202.
ACCESSION CS105031
VERSION CS105031.1 GI:67512962
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Selden, R.F., Borowski, M., Treco, D.A., Gillespie, F.P.,
Kinoshita, C.M. and Williams, M.D.
TITLE Production of human alpha-galactosidase A
JOURNAL Patent: EP 1538202-A 22 08-JUN-2005;
Transkaryotic Therapies, Inc. (US)
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LOCUS
DEFINITION Sequence 22 from patent US 6566099.
ACCESSION AR322465
VERSION AR322465.1 GI:33708230
KEYWORDS
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ORGANISM
REFERENCE 1
AUTHORS Selden, R.F., Borowski, M., Treco, D.A., Gillespie, F.P.,
Kinoshita, C.M. and Williams, M.D.
TITLE Production of human alpha-galactosidase A
JOURNAL Patent: US 6566099-A 22 20-MAY-2003;
Transkaryotic Therapies, Inc.; Cambridge, MA
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Db 65 AAGAGGCGCAGTGC 77

RESULT 11
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LOCUS
DEFINITION Sequence 22 from patent US 6395884.
ACCESSION AR372141
VERSION AR372141.1 GI:34609450
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Selden, R.F., Borowski, M., Gillespie, F.P., Kinoshita, C.M.,
Treco, D.A. and Williams, M.D.
TITLE Therapy for alpha-galactosidase a deficiency
JOURNAL Patent: US 6395884-A 22 28-MAY-2002;
Transkaryotic Therapies, Inc.; DE
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QY 95 GGGAGGCAGTGC 107
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Db 65 AAGAGGCGCAGTGC 77

RESULT 12
HUMGHPA
LOCUS
DEFINITION Human precursor growth hormone mRNA, 5' end.
ACCESSION M14398
VERSION M14398.1 GI:193158
KEYWORDS growth hormone.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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LOCUS      102190
DEFINITION Sequence 2 from Patent US 4859600.
ACCESSION 102190
VERSION    102190.1  GI:270293
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 80)
AUTHORS   Gray, G.L. and Heyneker, H.L.
TITLE      Recombinant procaryotic cell containing correctly processed human
           growth hormone
JOURNAL    Patent: US 4859600-A 2 22-AUG-1989;
           Genentech, Inc.; South San Francisco, CA
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LOCUS       CQ554646             65 bp      DNA
DEFINITION  Sequence 24281 from Patent WO0210449.
ACCESSION   CQ554646
VERSION     CQ554646.1   GI:41521073
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
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REFERENCE   1
            Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
            Oligonucleotide library for detecting rna transcripts and splice
            variants that populate a transcriptome
            Patent: WO 0210449-A 24281 07-FEB-2002;
            CompuGen Inc. (US)
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Db      8 TACAAGGTGGGAGTTGTGAAGCAAACTGAAACTGCCGCAATTAAAGGCCATCGGAG 62

RESULT 16

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CQ530857/c
 LOCUS CQ530857 65 bp DNA linear PAT 30-JAN-2004
 DEFINITION Sequence 492 from Patent WO0210449.
 ACCESSION CQ530857
 VERSION CQ530857.1 GI:41497121
 KEYWORDS Rattus norvegicus (Norway rat)
 SOURCE Rattus norvegicus
 ORGANISM Rattus norvegicus
 REFERENCE 1
 AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
 TITLE Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
 JOURNAL Patent: WO 0210449-A 492 07-FEB-2002;
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 Best Local Similarity 69.0%; Pred. No. 1.2e+05;
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 Qy 58 GGCACAGTCTCTTCGTTGACTGCTTACCCCGGGA 99
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 42 GTCACCTGCTCTTCTTGGTTAATCTGCTCAACCCCTTGGA 1
 RESULT 17
 CS001411/c
 LOCUS CS001411 75 bp DNA linear SYN 01-FEB-2005
 DEFINITION Sequence 172 from Patent WO2005005462.
 ACCESSION CS001411
 VERSION CS001411.1 GI:58423889
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Chan,A.C., Gordon,N.C., Kelley,R.F., Koehler,M.F. and
 Starovasmik,M.A.
 TITLE Blys antagonists and uses thereof
 JOURNAL Patent: WO 2005005462-A 20-JAN-2005;
 Genentech, Inc. (US)
 FEATURES source
 Location/Qualifiers
 1..75
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Clone 52,71"
 ORIGIN
 Query Match 12.8%; Score 21; DB 11; Length 75;
 Best Local Similarity 82.8%; Pred. No. 1.3e+05;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 3 TCGGCCACCTTTCATGAGGGGACTGGCA 31
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 72 TCCTCACCCGTTGATGAGGTGACAGGGCA 44
 RESULT 18
 CS063833
 LOCUS CS063833 50 bp DNA linear PAT 20-APR-2005
 DEFINITION Sequence 22 from Patent WO2005030963.
 ACCESSION CS063833
 VERSION CS063833.1 GI:62817056
 KEYWORDS

SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Dupraz,P. and Kobr,M.
 TITLE Leader sequences for use in production of proteins
 JOURNAL Patent: WO 2005030963-A 22 07-APR-2005;
 Applied Research Systems ARS Holding N.V. (AN)
 FEATURES source
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 1..50
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 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 ORIGIN
 Query Match 12.8%; Score 20.6; DB 6; Length 50;
 Best Local Similarity 67.4%; Pred. No. 1.8e+05;
 Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 Qy 72 CCTGGTTTGAATCTCTTACCCCGGGGAGGAGTGCAGCCAGC 114
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2 CCTGCTGTGCTCCCTGCTGCTGAGGAGGAGGAGCCGACAGC 44
 RESULT 19
 CQ534582
 LOCUS CQ534582 65 bp DNA linear PAT 30-JAN-2004
 DEFINITION Sequence 4217 from Patent WO0210449.
 ACCESSION CQ534582
 VERSION CQ534582.1 GI:41500846
 KEYWORDS Rattus norvegicus (Norway rat)
 SOURCE Rattus norvegicus
 ORGANISM Rattus norvegicus
 REFERENCE 1
 AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
 TITLE Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
 JOURNAL Patent: WO 0210449-A 4217 07-FEB-2002;
 Compugen Inc. (US)
 FEATURES source
 Location/Qualifiers
 1..65
 /organism="Rattus norvegicus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:10116"
 ORIGIN
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 Best Local Similarity 62.7%; Pred. No. 1.8e+05;
 Matches 32; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 Qy 40 CAGTCCCGAAGTTCTCAGGCACAGGTCTCTCTCTGTTGACTGCTCTTA 90
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 6 CAGTGAAGCAGATCTTCAGAGACAGACATCTCTCTTAGGACTCTCTCA 56
 RESULT 20
 CQ558604
 LOCUS CQ558604 65 bp DNA linear PAT 30-JAN-2004
 DEFINITION Sequence 28239 from Patent WO0210449.
 ACCESSION CQ558604
 VERSION CQ558604.1 GI:41525031
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 REFERENCE 1
 AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
 TITLE Oligonucleotide library for detecting rna transcripts and splice

variants that populate a transcriptome
Patent: WO 0210449-A 28239 07-FEB-2002;
CompuGen Inc. (US)
Location/Qualifiers
1. .65
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

ORIGIN
Query Match 12.6%; Score 20.6; DB 6; Length 65;
Best Local Similarity 67.4%; Pred. No. 1.8e+05;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 97 GAGGCGAGTGCAGCTGCAAGCCGCCAGTGAAGAACATC 139
|||||
DB 10 GGTGCACTGAAGTGTTCAGAGCACCATGGAGAGAACTTC 52
|||||

RESULT 21
LOCUS AF189414
DEFINITION Homo sapiens clone B301U T-cell receptor beta chain (TCRBV20S1)
mRNA, partial cds.
ACCESSION AF189414
VERSION AF189414.1 GI:6841695
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Soudeyns,H., Champagne,P., Holloway,C.L., Silvestri,G.U., Ringuelette,N., Samson,J., Lapointe,N. and Sekaly,R.P. Transient T cell receptor beta-chain variable region-specific expansions of CD4+ and CD8+ T cells during the early phase of pediatric human immunodeficiency virus infection: characterization of expanded cell populations by T cell receptor phenotyping J. Infect. Dis. 181 (1), 107-120 (2000) 10608757
AUTHORS Soudeyns,H., Champagne,P., Holloway,C.L., Silvestri,G.U., Ringuelette,N., Samson,J., Lapointe,N. and Sekaly,R.P. Direct Submission
TITLE Submitted (24-SEP-1999) Laboratoire d'immunologie, IRCM, 110 avenue Des Pins ouest, Montreal, Quebec H2W 1R7, Canada
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
Des Pins ouest, Montreal, Quebec H2W 1R7, Canada
FEATURES
source
1. .69
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="B301U"
<1. .>69
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/note="V(D)J region"
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/product="T-cell receptor beta chain"
/protein_id="AAF29201.1"
/db_xref="GI:6841696"
/translation="LLSDSGFYLCWSVYLTGELFF"

ORIGIN
Query Match 12.6%; Score 20.6; DB 8; Length 69;
Best Local Similarity 74.3%; Pred. No. 1.8e+05;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 66 TCCTCTCTGCTGTTGACTGCTTACCCCGGGGAG 100
|||||
DB 26 TCTGTCCCTGGAGTGTCTATCTTAACACCGGGGAG 60
|||||

RESULT 22
LOCUS CS001427/c
DEFINITION 75 bp DNA linear SYN 01-FEB-2005
ACCESSION Sequence 188 from Patent WO2005005462.
VERSION CS001427
KEYWORDS CS001427.1 GI:58423905
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Chan,A.C., Gordon,N.C., Kelley,R.F., Koehler,M.F. and Starovasinik,M.A.
TITLE Blys antagonists and uses thereof
JOURNAL Patent: WO 2005005462-A 20-JAN-2005;
Genentech, Inc. (US)
FEATURES
source
1. .75
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Clone 68"

ORIGIN
Query Match 12.6%; Score 20.6; DB 11; Length 75;
Best Local Similarity 62.7%; Pred. No. 1.8e+05;
Matches 32; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 3 TCGCCACCTTTGATGAGGGGACTGGGCGAGTCTAGACAGTCCGAGATTC 53
|||||
DB 72 TCTCCACCGGTGATGAGGTGACAGGGCACCAGCGCGAACCAGGAGATC 22
|||||

RESULT 23
LOCUS BOVBTB36/c
DEFINITION Bos taurus mRNA for T-cell receptor beta chain, diversity and joining regions.
ACCESSION D90135
VERSION D90135.1 GI:217465
KEYWORDS Bos taurus (cow)
SOURCE Bos taurus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE Tanaka,A., Ishiguro,N. and Shinagawa,M.
AUTHORS Sequence analysis of bovine T-cell receptor beta chain genes
TITLE Unpublished
JOURNAL These data kindly submitted in computer readable form by: Atsuko Tanaka
COMMENT Department of Veterinary Public Health
Obihiro University of Agriculture and Veterinary Medicine
Inada-cho
Obihiro, Hokkaido 080
Japan
Phone: 81-155-48-5111 x281.
Location/Qualifiers
1. .60
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="BTB36"
/cell_type="T cell"
<1. .>60
/note="unnamed protein product; T-cell receptor beta chain, diversity region and joining region"
/codon_start=1
/protein_id="BAA14163.1"
/db_xref="GI:217466"
/db_xref="IMG/IMG/LIGM:D90135"

FEATURES
source
81-155-48-5111 x281.
Location/Qualifiers
1. .60
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/cell_type="T cell"
<1. .>60
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/db_xref="GI:217466"
/db_xref="IMG/IMG/LIGM:D90135"

CDS

/translation="EADWGAARPDFGAGSWLTVV"

ORIGIN

	Query Match	12.4%	Score 20.4;	DB 4;	Length 60;
	Best Local Similarity	65.2%;	Pred. No. 2.1e+05;		
	. Matches	30;	Conservative	0;	Mismatches 16; Indels 0; Gaps 0;
Qy	107	CAGCCAGCTCGAAGCCCCACAGTCGAAACATCTGAGCTCAATCC	152		
Db	51	CAGCCAGCTCGCGCCCCGGAAGTCAGGGCGCGCTGCCCCCGAGTCC	6		

RESULT 24

CQ561327					PAT 30-JAN-2004
LOCUS	CQ561327	65 bp	DNA	linear	
DEFINITION	sequence 30962 from Patent WO0210449.				

ACCESSION CQ561327

VERSION C0561327.1 GI:41527754

KEYWORDS

SOURCE *Mus musculus* (house mouse)

ORGANISM

Mus musculus

Mus musculus (house mouse),

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus,

1
Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
Patent: WO 0210449-A 30962 07-FEB-2002;
Comugen Inc. (US)

FEATURES

source 1.65

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/organism="Mus musculus"

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/mol type="unassigned DNA"

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/db xref="taxon:10090"
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ORIGIN

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Best Local Similarity	65.2%;	Pred. No.	2.1e+05;				
Matches	30;	Conservative	0;	Mismatches	16;	Indels	0;

RESULT 25

LOCUS	SEQUENCE DEFINITION	77 bp	DNA	linear	PAT 19-JAN-2004
CQ055775	CQ055775	6595	from Patent WO0157270.		

ACCESSION C0055775

VERSION CO055775.1 GI:41030281

VERSION
KEYWORDS

KEYWORDS: Networks, Homo sapiens (human), SOURCE

SOURCE: Homo sapiens (human);
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1. Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nuclear acid probes useful for
analysis of gene expression in human breast and hbl 100 cells
Patent: WO 0157270-A 6595 09-AUG-2001;
JOURNAL

Aeomica, Inc. (US)

FEATURES

source 1: .77

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/mol type="unassigned DNA"
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/db xref="taxon:9606"
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/note="MAP TO AI.033380.10
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/HOC= HAF 10 AL033300:10
 EXPRESSED IN HRI.100 SIGNAL. =1 3

EXPRESSED IN HBL100, SIGNAL = 1.3
EST HUMAN HIT: W02144 1 EVALJIE 3 60e+00

SWISSPROT HIT: Q58016, EVALUE 5.40e+00"

ORIGIN

Query Match	12.4%;	Score 20.4;	DB 6;	Length 77;
Best Local Similarity	61.1%;	Pred. No. 2.1e+05;		
Matches 33;	Conservative	0;	Mismatches 21;	Indels 0;
Gaps	0;			

Qy	94	CGGGAGGGCAGTGCACCCAGCTGCAAGCCCCACAGTGAAGACATCTGAGCTCA	147
Db	1	CTGGGAGAGGGTGCACCCAGATTCAAGGCAGAGTTCGCTGGCTCTCTGGGATCA	54

Search completed: March 3, 2006, 08:38:47

Job time : 3435.27 secs

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM nucleic - nucleic search, using sw model
 Run on: March 3, 2006, 07:02:58 ; Search time 1070.86 Seconds
 (without alignments)
 1020.680 Million cell updates/sec

Title: US-10-655-801-3_COPY_14_177
 Perfect score: 164
 Sequence: 1 tctcgccaccttgatgag.....tcaaatccagataagtaca 164

Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 5180220

Minimum DB seq length: 0
 Maximum DB seq length: 80

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

Database : N_Geneseq_21.*
 1: Geneseqn1980s.*
 2: Geneseqn1990s.*
 3: Geneseqn2000s.*
 4: Geneseqn2001as.*
 5: Geneseqn2001bs.*
 6: Geneseqn2002as.*
 7: Geneseqn2002bs.*
 8: Geneseqn2003as.*
 9: Geneseqn2003bs.*
 10: Geneseqn2003cs.*
 11: Geneseqn2003ds.*
 12: Geneseqn2004as.*
 13: Geneseqn2004bs.*
 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	16.5	75	6	AAL45878
2	27	16.5	75	6	ABL54799 Modified
3	25.4	15.5	75	6	ABL54879
4	25.4	15.5	75	6	ABL54800 Modified
5	23.6	14.4	65	6	ABN53195
6	22	13.4	65	6	ABN31002
7	21.8	13.3	78	3	AAV31802
8	21.8	13.3	78	3	AAV70677 Human gro
9	21.8	13.3	78	6	AAV42076 Human gro
10	21.8	13.3	78	10	AAV60100 hGH signa
11	21.8	13.3	78	10	ADH54440 Human GH
12	21.8	13.3	78	13	ADH54440 Nucleotid
13	21.8	13.3	78	13	ADH54440 Polynucle
14	21.8	13.3	78	13	ADH54440 Signal pe
15	21.4	13.0	65	6	ABN51533 Mouse spl
16	21.2	12.9	65	6	ABN27744 Rat splc
17	21	12.8	21	2	AAQ79424
18	21	12.8	69	2	AAQ39611 H22V Ige
19	21	12.8	69	2	AAQ62599 DNA encod

75	14	ADW21434	Adw21434 Blys bind
76	6	ABL75541	AbL75541 Corn tass
77	14	ADZ00380	Adz00380 Human gro
78	6	ABN31469	Abn31469 Rat splc
79	6	ABN55491	Abn55491 Mouse spl
80	14	ADW21450	Adw21450 Blys bind
81	6	ABN58214	Abn58214 Mouse spl
82	7	AAI20896	Aai20896 Probe #10
83	7	ABA65968	Aba65968 Human foe
84	7	AAI46135	Aai46135 Probe #14
85	7	ABA48083	Aba48083 Human bre
86	7	ABA33059	Aba33059 Probe #11
87	7	AAK40120	Aak40120 Human bon
88	7	AAK14390	Aak14390 Human bra
89	7	ABS39705	Abs39705 Human liv
90	7	AAI06604	Aai06604 Probe #65
91	7	ABS14187	AbS14187 Human gen
92	9	ACI20052	AcI20052 Human mic
93	5	ABL01077	AbL01077 Human SNP
94	6	ABN50504	Abn50504 Human spl
95	7	AAI17684	Aai17684 Recombina
96	7	AAI17684	Aai17684 Recombina
97	7	AAI17682	Aai17682 Recombina
98	8	AAI37014	Aai37014 Human cdc
99	2	AAI37051	Aai37051 Human cdc
100	34	ADT62814	Adt62814 Human alic
101	35	ADT62797	Adt62797 Human alic
102	35	ADT62809	Adt62809 Human alic
103	35	ADT62815	Adt62815 Human alic
104	36	ADT62816	Adt62816 Human alic
105	36	ADT62813	Adt62813 Human alic
106	36	ADT62808	Adt62808 Human alic
107	37	ADT62810	Adt62810 Human alic
108	37	ADT62807	Adt62807 Human alic
109	37	ADT62812	Adt62812 Human alic
110	51	AAI73944	Aai73944 Human sll
111	6	ABN47778	Abn47778 Human spl
112	6	ABN45286	Abn45286 Human spl
113	6	ABN45275	Abn45275 Human spl
114	50	AAI29364	Aai29364 Human SNP
115	41	ABZ57521	Abz57521 IGF bindi
116	41	ABZ57522	Abz57522 IGF bindi
117	60	ABN33297	Abn33297 Human spl
118	61	ADT02481	Adt02481 Recombina
119	70	AAF56802	Aaf56802 VEGF rece
120	78	ADZ45968	Adz45968 DNA encod
121	43	AAZ65121	Aaz65121 Probe spe
122	43	AAZ65121	Aaz65121 Probe spe
123	43	ACA58245	Aac58245 Human PRO
124	43	ACA64175	Aca64175 Novel hum
125	43	ABX80634	Abx80634 Human sec
126	43	ACD44143	AcD44143 Human PRO
127	43	ABX79314	Abx79314 Human sec
128	43	ACA93335	AcA93335 Secreted
129	43	ABX81017	Abx81017 Novel hum
130	43	ACA92833	AcA92833 Secreted
131	43	ABX16917	Abx16917 Human PRO
132	43	ACA67772	AcA67772 Novel hum
133	43	ACA88221	AcA88221 Human sec
134	43	ACD81728	AcD81728 Human PRO
135	43	ADA37545	Ada37545 Human sec
136	43	ADA21231	Ada21231 Human sec
137	43	ADA10018	Ada10018 Human PRO
138	43	ADA17562	Ada17562 Human PRO
139	43	ADA27670	Ada27670 Human sec
140	43	ADA94250	Ada94250 Human sec
141	43	ADA38475	Ada38475 Human sec
142	43	ADA92596	Ada92596 Human sec
143	43	ACH65289	Ach65289 Human sec
144	43	ADA22157	Ada22157 Human sec
145	43	ACD39279	AcD39279 Human PRO
146	43	ADA06323	Ada06323 Human sec
147	43	ADA39016	Ada39016 Human sec
148	43	ADB96042	AdB96042 Human PRO

93 19.4 11.8 43 10 ADC57514 Adc57514 Human PRO
94 19.4 11.8 43 10 ADC54878 Adc54878 Human PRO
95 19.4 11.8 43 10 ADC11745 Adc11745 Human PRO
96 19.4 11.8 43 10 ADC56167 Adc56167 Human PRO
97 19.4 11.8 43 10 ADC07222 Adc07222 Human sec
98 19.4 11.8 43 10 ADC11212 Adc11212 Human sec
99 19.4 11.8 43 10 ADC14334 Adc14334 Secreted
100 19.4 11.8 43 10 ADD07866 Add07866 Human sec

ALIGNMENTS

RESULT 1

AAL45878

ID AAL45878 standard; DNA; 75 BP.

XX AC

XX AAL45878;

XX AC

XX 08-JUL-2002 (first entry)

XX DT

XX DE Modified acetylcholine receptor subunit alpha PCR primer #9.

XX KW

XX Insecticide; acetylcholine receptor; pharmaceutical; PCR; primer; ss.

XX OS

XX Synthetic.

XX FN

XX EP1184390-A2.

XX PD

XX 06-MAR-2002.

XX PF

XX 16-AUG-2001; 2001EP-00118963.

XX PR

XX 28-AUG-2000; 2000DE-01042177.

XX PS

XX (FARB) BAYER AG.

XX PA

XX Adamczewski M, Ebbinghaus-Kintscher U, Methfessel C, Schulte T;

XX PI

XX WPI; 2002-271035/32.

XX DR

XX New acetylcholine receptor subunit, useful for identifying plant-protection and therapeutic agents, comprises segment of insect subunit inserted into vertebrate subunit.

XX PT

XX PS

XX Example 1; Page 43; 52pp; German.

XX CC

XX The present invention relates to a modified acetylcholine receptor in which at least one amino acid, in the region of an alpha-subunit of a vertebrate acetylcholine receptor that is homologous with a 45 amino acid sequence, is replaced by an amino acid that is present at the identical position in the corresponding region of an alpha-subunit of an insect acetylcholine receptor. This is useful for identifying new plant-protection agents and pharmaceuticals (for human or veterinary medicine), i.e. modulators of insect nicotinic receptors, for use as e.g. insecticides. The present sequence is a PCR primer for a modified acetylcholine receptor alpha subunit of the invention

XX CC

XX SQ

Sequence 75 BP; 17 A; 20 C; 22 G; 16 T; 0 U; 0 Other;

Query Match 16.5%; Score 27; DB 6; Length 75;

Best Local Similarity 60.0%; Pred. No. 60;

Matches 45; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 18 GAGGGAGCTGGCGAGTCTTAGACAGTCCCGAAGTTCTCAAGGCACAGGTCTCTTCCTGGT 77

Db 1 GCGGGAGTGGGTCTATCTTAGAAGTCCCGCGCGTTTCGACGAAAGTTTATACATGCT 60

Qy 78 TTGACTGCTCTTACC 92

Db 61 GCGACGAGCCCTACC 75

RESULT 2

ABL54799

ID ABL54799 standard; DNA; 75 BP.

XX AC

XX ABL54799;

XX AC

XX 13-JUN-2002 (first entry)

XX DT

XX DE Modified hen ACR subunit alpha 4 mutagenic oligo SEQ ID NO 16.

XX KW

XX Acetylcholine; receptor; ACR; subunit alpha; insect; insecticide; hen; plant-protection agent; veterinary; medicine; nicotinic receptor; ss.

XX OS

XX Synthetic.

XX PN

XX EP1184391-A2.

XX PD

XX 06-MAR-2002.

XX PF

XX 24-AUG-2001; 2001EP-00119704.

XX PR

XX 28-AUG-2000; 2000DE-01042177.

XX PS

XX (FARB) BAYER AG.

XX PA

XX Adamczewski M, Ebbinghaus-Kintscher U, Methfessel C, Schulte T;

XX PI

XX WPI; 2002-271036/32.

XX DR

XX New acetylcholine receptor subunit, useful for identifying plant-protection and therapeutic agents, comprises a segment of insect subunit inserted into vertebrate subunit.

XX PT

XX PS

XX Example 1; Page 10; 46pp; German.

XX CC

XX The invention relates to modified acetylcholine receptor (ACR) subunit (I) in which at least one amino acid (aa), in the region of an alpha-subunit of a vertebrate ACR that is homologous with a ACR of Torpedo californica (AB008882), is replaced by an aa that is present at the identical position in the corresponding region of an alpha-subunit of an insect ACR. (II), ACR containing them and the nucleic acid (II) encoding them, are useful for identifying new plant-protection agents and pharmaceuticals (for human or veterinary medicine), i.e. modulators (agonists or antagonists) of the properties of insect nicotinic receptors, e.g. insecticides. The present sequence is that of a mutagenic oligonucleotide used to generate the modified hen ACR alpha 4 subunit of the invention. The modified hen ACR alpha 4 subunit is generated by insertion of part of the nicotinic ACR alpha 1 subunit from the insect Heliothis virescens into the hen ACR alpha 4 subunit (Genbank AJ250361)

XX CC

XX SQ

Sequence 75 BP; 17 A; 20 C; 22 G; 16 T; 0 U; 0 Other;

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

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XX CC

XX CC

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XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

XX CC

DE	Modified acetylcholine receptor subunit alpha PCR primer #10.
XX	Insecticide; acetylcholine receptor; pharmaceutical; PCR; primer; ss.
KW	Synthetic.
OS	
XX	
PN	EP1184390-A2.
XX	
PD	06-MAR-2002.
XX	
PF	16-AUG-2001; 2001EP-00118863.
XX	
PR	28-AUG-2000; 2000DE-01042177.
XX	(FARB) BAYER AG.
XX	
PI	Adamczewski M, Ebbinghaus-Kintscher U, Methfessel C, Schulte T;
XX	WFI; 2002-271035/32.
XX	
PT	New acetylcholine receptor subunit, useful for identifying plant-
PT	protection and therapeutic agents, comprises segment of insect subunit
PT	inserted into vertebrate subunit.
XX	
PS	Example 1; Page 44; 52pp; German.
XX	
CC	The present invention relates to a modified acetylcholine receptor in
CC	which at least one amino acid, in the region of an alpha-subunit of a
CC	vertebrate acetylcholine receptor that is homologous with a 45 amino acid
CC	sequence, is replaced by an amino acid that is present at the identical
CC	position in the corresponding region of an alpha-subunit of an insect
CC	acetylcholine receptor. This is useful for identifying new plant-
CC	protection agents and pharmaceuticals (for human or veterinary medicine),
CC	i.e. modulators of insect nicotinic receptors, for use as e.g.
CC	insecticides. The present sequence is a PCR primer for a modified
CC	acetylcholine receptor alpha subunit of the invention
XX	
SQ	Sequence 75 BP; 16 A; 22 C; 20 G; 17 T; 0 U; 0 Other;
	Query Match 15.5%; Score 25.4; DB 6; Length 75;
	Best Local Similarity 58.7%; Pred.No.2.le+02;
	Matches 44; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY	18 GAGGGGACTGGCGAGTTCTAGACAGTCCCGAAGTTCTCAAGGCACAGTCTCTTCCTGGT 77
Db	75 GCGGGAGTGGGTCATCATTTGAAGTCCGGCCGTTCGCACGAAAGTTTTATACATGCT 16
QY	78 TTGACTGTCTCTACC 92
Db	15 GCGACGAGCCCTACC 1
	RESULT 4
	ABL54800/c
ID	ABL54800 standard; DNA; 75 BP.
XX	
AC	ABL54800;
AC	
DT	13-JUN-2002 (first entry)
XX	
DE	Modified hen ACR subunit alpha 4 mutagenic oligo SEQ ID NO 17.
XX	
KW	Acetylcholine; receptor; ACR; subunit alpha; insect; insecticide; hen;
KW	plant-protection agent; veterinary; medicine; nicotine receptor; ss.
XX	Synthetic.
OS	
XX	
PN	EP1184391-A2.
XX	
PD	06-MAR-2002.
XX	
PF	24-AUG-2001; 2001EP-00119704.
XX	

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PR 28-AUG-2000; 2000DE-01042177.
XX (FARB ) BAYER AG.
XX
XX Adamczewski M, Ebbinghaus-Kintscher U, Methfessel C, Schulte T;
XX
XX WPI; 2002-271036/32.
XX
XX New acetylcholine receptor subunit, useful for identifying plant-
PT protection and therapeutic agents, comprises a segment of insect subunit
PT inserted into vertebrate subunit.
XX
XX Example 1; Page 10; 46pp; German.
XX
XX The invention relates to modified acetylcholine receptor (ACR) subunit
CC (I) in which at least one amino acid (aa), in the region of an alpha-
CC subunit of a vertebrate ACR that is homologous with a ACR of Torpedo
CC californica (AB08882), is replaced by an aa that is present at the
CC californica position in the corresponding region of an alpha-subunit of an
CC insect ACR. (I), ACR containing them and the nucleic acid (II) encoding
CC them, are useful for identifying new plant-protection agents and
CC pharmaceuticals (for human or veterinary medicine), i.e. modulators
CC (agonists or antagonists) of the properties of insect nicotinic
CC receptors, e.g. insecticides. The present sequence is that of a mutagenic
CC oligonucleotide used to generate the modified hen ACR alpha 4 subunit of
CC the invention. The modified hen ACR alpha 4 subunit is generated by
CC insertion of part of the nicotinic ACR alpha 1 subunit from the insect
CC Heliothis virescens into the hen ACR alpha 4 subunit (Genbank AJ250361)
XX
XX Sequence 75 BP; 16 A; 22 C; 20 G; 17 T; 0 U; 0 Other;
SQ
Query Match 15.5%; Score 25.4; DB 6; Length 75;
Best Local Similarity 58.7%; Pred. No. 2.1e+02;
Matches 44; Conservative 0; Mismatches 31; Indels 0; Gaps 0
QY 18 GAGGGGAGCTGGGAGTTCTAGACAGTCCCGAAGTCTCAAGGCACAGTCTCTTCTGTGT 77
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
75 GCGGGGAGTGGGTCATCATTTGAAGTCCGCGCGTTCGCACACGAAAAGTTTATACATGCT 16
QY 78 TTGACTGTCTCTTACC 92
Db ||||| ||||| ||||| |||||
15 GCGACGAGCCCTACC 1
RESULT 5
ABN53195
ID ABN53195 standard; DNA; 65 BP.
XX
XX AC ABN53195;
XX
XX 15-JUL-2002 (first entry)
XX
XX Mouse spliced transcript detection oligonucleotide SEQ ID NO:25943.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Mus musculus.
XX
XX WO200210449-A2.
XX
XX 07-FEB-2002.
XX
XX 20-JUL-2001; 2001WO-IB001903.
XX
XX 28-JUL-2000; 2000US-0221607P.
XX
XX 02-MAY-2001; 2001US-0287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
XX WPI; 2002-257383/30.
XX

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[illegible]

XX	(TRAN-) TRANSKARYOTIC THERAPIES INC.
PA	Selden RF, Borowski M, Gillespie FP, Kinoshita CM, Treco DA;
XX	Williams MD;
PI	WPI; 1998-207375/18.
XX	P-PSDB; AAW37989.
DR	Treatment of alpha-galactosidase A deficiency in, e.g. Fabry disease --
DR	comprises use of genetically modified human cells that express alpha-
PT	galactosidase.
PT	Disclosure; Fig 11; 78pp; English.
XX	This is the nucleotide sequence of the human growth hormone signal
FS	peptide, used in the method of the invention, which involves the
XX	production of genetically modified human cells that express alpha-
CC	galactosidase. The cultured human cells can be used for the production of
CC	glycosylated human alpha-gal A and can be used for the treatment of
CC	patients with an alpha-gal A deficiency, e.g. Fabry disease (an X-linked
CC	inherited lysosomal storage disease)
XX	Sequence 78 BP; 8 A; 28 C; 23 G; 19 T; 0 U; 0 Other;
QQ	
CC	Query Match 13.3%; Score 21.8; DB 2; Length 78;
CC	Best Local Similarity 56.2%; Pred. No. 3.4e+03;
CC	Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY	35 CTACACAGTCCCGAAGTTCTCAAGGCACAGGTCTTCCTCGGTTTGACTGTCCTTACCCC 94
Db	5 CTACAGGCTCCGGACGTCCTGCTCCTGGCTTTTGGCTCTGCTGCCCTGGCTTC 64
QY	95 GGGGAGGCGCATGC 107
Db	65 AAGAGGCGCATGC 77
RESULT 8	
AAA70677	
ID	AAA70677 standard; DNA; 78 BP.
AC	AAA70677;
XX	15-DEC-2000 (first entry)
DT	Human growth hormone signal peptide coding sequence.
DE	Nephrotropic; gene therapy; alpha-galactosidase A deficiency; ss;
KX	Fabry disease; secretion; human growth hormone; hGH; signal peptide;
KW	enzyme replacement therapy.
KW	Homo sapiens.
OS	US6083725-A.
XX	04-JUL-2000.
PD	12-SEP-1997; 97US-00928881.
PF	13-SEP-1996; 96US-0026041P.
PR	(TRAN-) TRANSKARYOTIC THERAPIES INC.
XX	Kinoshita CM, Treco DA, Williams MD, Selden RF, Borowski M;
PA	Gillespie FP;
XX	WPI; 2000-464341/40.
XX	P-PSDB; AAB15386.
DR	New DNA comprising a human growth hormone signal peptide and human alpha-
DR	galactosidase A polypeptide and cells expressing the DNA, useful for
PT	treating Fabry disease and in vitro protein production for enzyme

The present invention provides a new, effective and efficient method for producing multimeric proteins in the egg-laying (avian) or milk producing animals. The multimeric proteins include associated multimeric proteins (two or more associated polypeptides) and multivalent multimeric proteins (a single polypeptide is encoded by multiple genes). The expression and formation of a multimeric protein is achieved by administering a polynucleotide cassette containing genes of interest (for example prolinsulin, antibodies, cytokines, etc.). The polynucleotide cassettes are administered to egg-laying or milk producing animals to create the transgenic animals. Several different signal sequences and promoters can be used to achieve the deposition of the multimeric protein in the egg or milk. The transposon based vector has been used for the incorporation of polynucleotide cassettes into the genomic DNA. The polynucleotide cassette may additionally contain multiple pro sequences, prepro sequences, cecropin prepro sequences and cleavage sites. Each gene encodes a polypeptide which forms part of a multimeric protein. The pro portion of the sequences has been used to facilitate appropriate processing, expression and formation of multimeric proteins. These multimeric proteins can be produced much more efficiently and

PA (LOU) UNIV LOUISIANA STATE & AGRIC & MECH COLL.

PI Cooper RK, Fioretti WC, Cadd GG;

XX WPI; 2004-581003/56.

XX New polynucleotide (transposon-based vector) cassette comprising gene of
PT interest operably linked to a cecropin prepro sequence, is useful in
PT producing vaccines to protect an individual against infectious diseases.

XX Disclosure; SEQ ID NO 28; 155pp; English.

XX The patent discloses novel, effective and efficient method of producing
CC multimeric proteins, antibodies using transposon-based vectors, in
CC transgenic individuals. These proteins can be used as a vaccine.
CC Immunising individuals with such compositions, comprising vaccines is
CC capable of generating an immune response, to prevent or ameliorate the
CC severity of a disease. The invention provides polynucleotide cassettes
CC containing at least one gene of interest and one or more pro
CC polynucleotide sequence, where in each gene of interest are operably-
CC linked to a pro nucleotide sequence of at least one gene of interest. The
CC transposon-based vector comprises the polynucleotide and further
CC comprises a transposase gene operably linked to a first promoter and
CC where the first promoter comprises a modified Kozak sequence, two or more
CC genes of interest are each operably-linked to one or more additional
CC promoters, and two or more genes of interest and their operably-linked
CC promoters are flanked by transposase insertion sequences recognized by a
CC transposase encoded by the transposase gene. Many diseases and disease
CC causing organisms can be targets of the vaccine of the present invention.
CC Some of these include, anthrax, botulism, brucellosis, glanders, Q fever,
CC plague, shigellosis, small pox, tularemia, viral encephalitis, typhus
CC fever, viral hemorrhagic fever, etc. The preferred animal for production
CC of protein is a bird or a mammal. The egg or milk of these animals
CC comprises the multimeric protein encoded by the isolated polynucleotide
CC of the invention. Hence, these proteins are endowed with varied
CC properties and are antibacterial, anti viral, antimicrobial, anti-
CC inflammatory, and neuroprotective in nature. The sequence presented here
CC is the polynucleotide encoding signal peptide sequence.

XX Sequence 78 BP; 8 A; 28 C; 23 G; 19 T; 0 U; 0 Other;

Query Match 13.3%; Score 21.8; DB 13; Length 78;
Best Local Similarity 56.2%; Pred. No. 3.4e+03;
Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 35 CTAGACAGTCCCGAGTCTCTCAGGACAGGTCTCTCTGTTGACTGCTCTTACCC 94
DB 5 CTACAGGCTCCCGAGCTCCCTGCTCTCTGCTTTTGGCTCTGCTCTGCTGCTTC 64

QY 95 GGGGAGGCACTGC 107

DB 65 AAGAGGGCAGTGC 77

RESULT 14

ID ADU66735 standard; DNA; 78 BP.

XX ADU66735;

DT 10-FEB-2005 (first entry)

DE Signal peptide encoding polynucleotide, seqid:28.

XX Multimeric protein; transgenic; leukaemia inhibitory factor;
KW tumour necrosis factor; angiotensin; bone morphogenetic protein;
KW adrenomedullin; calcitonin; amyloid; calcitonin gene-related peptide;
KW insulin; growth hormone releasing hormone; GHRH;
KW granulocyte-macrophage colony stimulating factor; G-CSF; albumin;
KW apolipoprotein; anti-hepatitis antibody; anti-cytomegalovirus antibody;
KW anti-rabies antibody; antivenin latrodectus; thyrotropin;
KW glial cell line-derived neurotrophic factor;
KW antimetastatic cancer antibody; ss.

XX Unidentified.
XX US2004235011-A1.

XX 25-NOV-2004.

XX 24-DEC-2003; 2003US-00746943.

XX 26-JUN-2002; 2002US-0392415P.

XX 21-JAN-2003; 2003US-0441377P.

XX 21-JAN-2003; 2003US-0441381P.

XX 21-JAN-2003; 2003US-0441392P.

XX 21-JAN-2003; 2003US-0441405P.

XX 21-JAN-2003; 2003US-0441477P.

XX 21-JAN-2003; 2003US-0441502P.

XX 26-JUN-2003; 2003US-00609019.

XX (COOP/) COOPER R K.

XX (FIOR/) FIORETTI W C.

XX (CADD/) CADD G G.

XX Cooper RK, Fioretti WC, Cadd GG;

XX WPI; 2004-832941/82.

XX Novel isolated polynucleotide comprising genes of interest e.g., anti-
PT her2, and pro nucleotide sequences, useful for producing multimeric
PT proteins such as antimetastatic cancer antibodies, in animals.
XX Disclosure; SEQ ID NO 28; 107pp; English.
XX The invention relates to a polynucleotide sequence comprising genes of
CC interest and pro nucleotide sequences. The invention also relates to a
CC method for producing multimeric protein or multivalent multimeric
CC protein. The polynucleotide sequence of the invention is useful for
CC producing multimeric proteins in a transgenic individual such as egg-
CC laying animal or a milk-producing animal. It is useful in producing
CC multimeric proteins or proteins such as leukaemia inhibitory factor,
CC tumour necrosis factor alpha and beta, angiotensin, bone morphogenetic
CC proteins, adrenomedullin, calcitonin, amyloid, calcitonin gene-related
CC peptide, insulin, growth hormone releasing hormone (GHRH), granulocyte-
CC macrophage colony stimulating factor (G-CSF), albumin, apolipoprotein,
CC anti-hepatitis antibody, anti-cytomegalovirus antibody, anti-rabies
CC antibody, antivenin latrodectus, thyrotropin, glial cell line-derived
CC neurotrophic factor, antimetastatic cancer antibody etc. The present
CC sequence is a signal peptide encoding polynucleotide. This sequence is
CC used in the production of multimeric proteins.

XX Sequence 78 BP; 8 A; 28 C; 23 G; 19 T; 0 U; 0 Other;

Query Match 13.3%; Score 21.8; DB 13; Length 78;
Best Local Similarity 56.2%; Pred. No. 3.4e+03;
Matches 41; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 35 CTAGACAGTCCCGAGTCTCTCAGGACAGGTCTCTCTGTTGACTGCTCTTACCC 94
DB 5 CTACAGGCTCCCGAGCTCCCTGCTCTCTGCTTTTGGCTCTGCTCTGCTGCTTC 64

QY 95 GGGGAGGCACTGC 107

DB 65 AAGAGGGCAGTGC 77

RESULT 15

ID ABN51533 standard; DNA; 65 BP.

XX ABN51533;

DT 15-JUL-2002 (first entry)

DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:24281.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX Mus musculus.
XX WO200210449-A2.
XX 07-FEB-2002.
XX 20-JUL-2001; 2001WO-IB001903.
XX 28-JUL-2000; 2000US-0221607P.
XX 02-MAY-2001; 2001US-0287724P.
XX (COMP-) COMPUGEN INC.
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX WPI; 2002-257383/30.
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX Example 1; SEQ ID NO 24281; 47pp; English.
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridizing selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 65 BP; 23 A; 12 C; 20 G; 10 T; 0 U; 0 Other;
Query Match 13.0%; Score 21.4; DB 6; Length 65;
Best Local Similarity 61.8%; Pred. No. 4.4e+03;
Matches 34; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
*QY 89 TACCCGGGAGCAGTGCAGCCAGTGCAGCCAGTGCAGCCAGTGCAGCCAGTGCAG 143
DB 8 TACAGGTGGAGTTGTGAAGCAAACTGAACCTGCCGCAATTAAGGCCATCGGAG 62
RESULT 16
ABN27744/C
ID ABN27744 standard; DNA; 65 BP.
XX AC
XX ABN27744;
XX 15-JUL-2002 (first entry)
XX DE Rat spliced transcript detection oligonucleotide SEQ ID NO:492.
XX

XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX Rattus norvegicus.
XX WO200210449-A2.
XX 07-FEB-2002.
XX 20-JUL-2001; 2001WO-IB001903.
XX 28-JUL-2000; 2000US-0221607P.
XX 02-MAY-2001; 2001US-0287724P.
XX (COMP-) COMPUGEN INC.
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX WPI; 2002-257383/30.
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX Example 1; SEQ ID NO 492; 47pp; English.
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridizing selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 65 BP; 28 A; 9 C; 20 G; 8 T; 0 U; 0 Other;
Query Match 12.9%; Score 21.2; DB 6; Length 65;
Best Local Similarity 69.0%; Pred. No. 5.1e+03;
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 58 GCACAGGTCTCTCTCTGTTGAGTGTCTTACCCCGGGA 99
DB 42 GTCACTGTCTCTCTCTGTTGAGTGTCTTACCCCGGGA 1
RESULT 17
AAQ79424
ID AAQ79424 standard; DNA; 21 BP.
XX AC
XX AAQ79424;
XX 25-MAR-2003 (revised)
XX 03-JUN-1995 (first entry)
XX DE PCR primer no. 12 based on human hepatocyte inducible nitric oxide
XX synthase (iNOS) cDNA.

XX Nitric oxide synthase; diabetes mellitus; PCR primer; ss.
 KW Synthetic.
 OS
 PN WO9424269-A1.
 XX
 XX 27-OCT-1994.
 XX
 XX 11-APR-1994; 94WO-DK000146.
 XX
 XX 16-APR-1993; 93DK-00000433.
 XX
 XX (NOVO) NOVO-NORDISK AS.
 XX
 XX Karlsen AE;
 XX
 XX WPI; 1994-341851/42.
 XX
 XX New DNA encoding inducible pancreatic islet nitric oxide synthase - and
 PT related vectors and transformed cells, useful for identifying specific
 PT inhibitors for treatment or prevention of insulin dependent diabetes
 PT mellitus.
 XX
 XX Example; Page 25; 36pp; English.
 PS
 CC Human islets were incubated in a mixture of IL-1, TNF-alpha and IFN-
 CC gamma. The human islet iNOS was cloned by RT-PCR on the isolated mRNA
 CC with primers based on the human hepatocyte sequence. The sequence of the
 CC primers is given in AAQ79424 and AAQ79425. The clone human islet iNOS was
 CC sequenced. The 5' UTR and translated human islet iNOS is given in
 CC AAQ79426, and the 3' end in AAQ79427. (Updated on 25-MAR-2003 to correct
 CC PN field.)
 XX
 XX Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 12.8%; Score 21; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AGTTCTCAAGGCACAGGTCTC 69
 DB 1 AGTTCTCAAGGCACAGGTCTC 21

RESULT 18
 AAQ39611
 ID AAQ39611 standard; DNA; 69 BP.
 AC
 AC AAQ39611;
 XX
 XX 25-MAR-2003 (revised)
 DT 12-OCT-1993 (first entry)
 XX
 XX H22V IGE - IGE Fc receptor binding effector peptide DNA.
 DE
 XX Surface protein; influenza A virus; vaccine; treatment; trigger site;
 KW allergic reactions; prevention; haemagglutinin surface protein;
 KW HA-IGE (HA-H22V); immunoglobulin; ds.
 XX
 XX Synthetic.
 OS
 XX EP546787-A2.
 PN
 XX 16-JUN-1993.
 PD
 XX 07-DEC-1992; 92EP-00311146.
 PF
 XX 11-DEC-1991; 91US-00805105.
 PR
 XX (AMHP) AMERICAN HOME PROD CORP.
 PA
 XX Hung PP, Lee SL, Kalyan NK;
 XX
 XX WPI; 1997-107145/10.

XX WPI; 1993-190138/24.
 DR P-PSDB; AAR37812.
 XX
 XX New DNA encoding haemagglutinin surface protein of influenza A virus and
 PT corresp. polypeptide - useful as a vaccine against HIV infection and
 PT allergic reactions.
 XX
 XX Example; Page 13; 17pp; English.
 PS
 XX
 CC The sequence is that encoding peptide H22V which contains an epitope
 CC corresponding to amino acids 497-506 of the human IGE heavy chain. The
 CC epitope is that of the effector or trigger site for the binding of IGE to
 CC the IGE Fc receptor and is located in the CH4 domain. The sense strand of
 CC the DNA overhangs the antisense strand by 4 bases at the 3' end, and the
 CC antisense strand overhangs the 5' end of the sense strand by the sequence
 CC CCGG. The sequence can be inserted into a nucleotide sequence encoding an
 CC influenza A virus haemagglutinin (HA) surface protein having five
 CC immunodominant antigenic sites into which the epitope encoding sequence
 CC is inserted. This can be used in the prodn. of the HA-IGE (HA-H22V)
 CC epitope which can be used in a vaccine for preventing or treating
 CC allergic reactions. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 69 BP; 19 A; 21 C; 15 G; 14 T; 0 U; 0 Other;

Query Match 12.8%; Score 21; DB 2; Length 69;
 Best Local Similarity 62.3%; Pred. No. 6.1e+03;
 Matches 33; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 30 CAGTTCTAGACAGTCCCGAAGTTCTCAAGGCACAGGTCTCTCTCTCGTTTGAC 82
 DB 3 CAGTACTACAGCCCCCGCAAAACCAAGGATCAGGATCTTTGTATTCTCAC 55

RESULT 19
 AAT62599

ID AAT62599 standard; DNA; 69 BP.
 XX
 AC AAT62599;
 XX

DT 25-MAR-2003 (revised)
 DT 12-MAY-1997 (first entry)
 XX
 XX DNA encoding human IGE heavy chain effector site epitope H22V.

KW IGE; haemagglutinin; HA; influenza A; surface protein; immunoglobulin;
 KW epitope; vaccine; antigen; ds.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FH CDS 1..66
 FT /*tag= a
 FT misc_feature 1
 FT /*tag= c
 FT /note= "complementary strand has 3' overhang of 5'-GGCC"
 FT misc_feature 67..69
 FT /*tag= b
 FT /note= "5' overhang"
 XX
 PN US5591823-A.
 XX
 XX 07-JAN-1997.
 PD
 XX 17-DEC-1993; 93US-00169813.
 PF
 XX 11-DEC-1991; 91US-00805105.
 PR
 XX (AMHP) AMERICAN HOME PROD CORP.
 PA
 XX Kalyan NK, Lee SL, Hung PP;
 XX
 XX WPI; 1997-107145/10.


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XX Novel purified corn tassel-derived polynucleotide useful for determining
PT altered gene expression, to recover regulatory elements and to follow
PT inheritance of desirable characteristics through hybrid breeding
PT programs.
XX
PS Claim 1; SEQ ID NO 4915; 201pp; English.
XX
CC The present sequence describes a purified corn tassel-derived
CC polynucleotide sequence (cdps) comprising a nucleic acid sequence
CC selected from those given in ABL70627 to ABL76833. The cdps sequences
CC encode corn tassel-derived polypeptides (CDPs). The cdps sequences (1)
CC can be used for determining altered gene expression, to recover
CC regulatory elements and to follow inheritance of desirable
CC characteristics through hybrid breeding programs. (1) are also useful in
CC the evaluation, and alteration of desired characteristics associated with
CC growth and development, disease resistance, environmental adaptability,
CC quality and yield, and as molecular markers for studying inheritance of
CC multigene traits in a plant breeding program. (1) can be used to produce
CC a tassel-specific profile of gene transcription, a transcript image, to
CC clone regulatory elements for use in transformation vectors, to express a
CC polypeptide, to identify, isolate or extend identical or related corn
CC tassel nucleic acid sequences from DNA libraries, in nucleic acid
CC hybridisation or amplification technologies, as query sequences to
CC determine homology of known sequences, as probe for use in Southern or
CC Northern hybridisation, and to identify the presence of and/or to
CC determine the degree of similarity between two (or more) nucleic acid
CC sequences
XX
SQ Sequence 67 BP; 18 A; 17 C; 15 G; 15 T; 0 U; 2 Other;
Query Match 12.7%; Score 20.8; DB 6; Length 67;
Best Local Similarity 62.0%; Pred. No. 7e+03;
Matches 31; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 105 TGCAGCCAGCTGCAAGCCACACAGTGAAGAACATCTGAGCTCAATCCAG 154
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 16 TTCAGACACCGGCAAGCAGCTCATTCAGATCNAITGAGTCCGATACNG 65

RESULT 22
ADZ00380
ID ADZ00380 standard; DNA; 50 BP.
XX
AC ADZ00380;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human growth hormone signal peptide primer #2.
XX
KW murine; immunoglobulin; signal peptide;
KW tissue-type plasminogen activator; tPA; pre-propeptide; human;
KW fusion protein; secretion; protein processing; ss; primer; primer.
XX
OS Homo sapiens.
XX Synthetic.
XX
PN WO2005030963-A1.
XX
PD 07-APR-2005.
XX
PF 24-SEP-2004; 2004WO-EP052302.
XX
PR 26-SEP-2003; 2003EP-00103580.
XX
PR 29-SEP-2003; 2003US-0506939P.
XX
PA (1STF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI Dupraz P, Kobr M;
XX
DR WPI; 2005-273383/28.
XX
PT New DNA construct comprising a sequence encoding an immunoglobulin signal

```

```

PT peptide (SP)-tissue-type plasminogen activator (tPA) pre-propeptide,
PT comprising an immunoglobulin SP fused to a tPA propeptide, useful for
PT producing polypeptides.
XX
PS Example 1; SEQ ID NO 22; 44pp; English.
XX
CC This sequence represents a primer which was used in the amplification of
CC a human growth hormone signal peptide which was used for comparison with
CC the DNA construct of the invention. The DNA construct of the invention
CC comprises a sequence encoding an immunoglobulin signal peptide (IGSP)-
CC tissue-type plasminogen activator (tPA) pre-propeptide comprising an IGSP
CC fused to a tPA propeptide. The tPA sequence is preferably a human tPA
CC where the carboxyl-terminal extremity of the tPA propeptide consists of
CC amino acids Arg-Xaa-Arg-Arg. The DNA construct of the invention encodes a
CC fusion polypeptide comprising the IGSP-tPA pre-propeptide fused to a
CC polypeptide of interest. The DNA construct further comprises a signal
CC sequence fused to the tPA propeptide. The DNA construct encodes a fusion
CC polypeptide comprising the tPA propeptide fused to a polypeptide of
CC interest. The DNA construct is useful for producing polypeptide of
CC interest. The DNA constructs are at least 2 fold more efficient in
CC promoting secretion and processing of proteins of interest than prior art
CC leader sequences.
XX
SQ Sequence 50 BP; 5 A; 17 C; 20 G; 8 T; 0 U; 0 Other;
Query Match 12.6%; Score 20.6; DB 14; Length 50;
Best Local Similarity 67.4%; Pred. No. 7.4e+03;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 72 CCTGCTTTGACTGTCTTACCCCGGGAGGCGAGTCGAGCGCAGC 114
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 2 CCTGCTGTGCTGCCCTGCTGCGAGGAGGCGCGACAGC 44

RESULT 23
ABN31469
ID ABN31469 standard; DNA; 65 BP.
XX
AC ABN31469;
XX
DT 15-JUL-2002 (first entry)
XX
DE Rat spliced transcript detection oligonucleotide SEQ ID NO:4217.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Rattus norvegicus.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
XX
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
PS Example 1; SEQ ID NO 4217; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-

```

CC)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises several
 CC oligonucleotides, each capable of hybridising selectively to a set of
 CC messenger RNAs transcribed from a given transcription unit of the genome,
 CC which encodes one or more messenger RNA splice variants. The
 CC oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterising the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a particular
 CC biological or pathological state, and so allowing the detection of tissue
 CC - and pathology-specific genes such as those genes only expressed in
 CC specific tissue under a specific pathological condition; to detect
 CC developmental specific genes; and to detect RNA transcripts and splice
 CC variants of a transcriptome of a patient suffering from a particular
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
 CC rats, humans and mice, which are used in the exemplification of the
 CC present invention. N.B. The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 65 BP; 20 A; 16 C; 15 G; 14 T; 0 U; 0 Other;

Query Match 12.6%; Score 20.6; DB 6; Length 65;
 Best Local Similarity 62.7%; Pred. No. 8.1e+03;
 Matches 32; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 40 CAGTCCCGAGTCTTCAAGCAGCAGGTCTCTCTCTGTTGACTGTCCTTA 90
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 Db 6 CAGTGAAGCAGATCTTCAGAGCAGACTCACTCTCTTAGGAACTCTCTCA 56

RESULT 24
 ABN55491
 ID ABN55491 standard; DNA; 65 BP.
 XX
 AC ABN55491;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:28239.
 XX
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX
 OS Mus musculus.
 XX
 PN WO200210449-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 20-JUL-2001; 2001WO-1B001903.
 XX
 PR 28-JUL-2000; 2000US-0221607P.
 PR 02-MAY-2001; 2001US-0287724P.
 XX
 PA (COMP-) COMPUEN INC.
 XX
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 XX
 DR WPI; 2002-257383/30.
 XX
 PT New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a
 PT genome, useful for detecting tissue-, pathology-, and developmental-
 PT specific genes.
 XX
 PS Example 1; SEQ ID NO 28239; 47pp; English.
 XX
 PS The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
 CC)transcriptome comprises messenger RNAs transcribed from multiple

CC transcription units that populate a genome. The library comprises several
 CC oligonucleotides, each capable of hybridising selectively to a set of
 CC messenger RNAs transcribed from a given transcription unit of the genome,
 CC which encodes one or more messenger RNA splice variants. The
 CC oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterising the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a particular
 CC biological or pathological state, and so allowing the detection of tissue
 CC - and pathology-specific genes such as those genes only expressed in
 CC specific tissue under a specific pathological condition; to detect
 CC developmental specific genes; and to detect RNA transcripts and splice
 CC variants of a transcriptome of a patient suffering from a particular
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
 CC rats, humans and mice, which are used in the exemplification of the
 CC present invention. N.B. The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 65 BP; 22 A; 14 C; 17 G; 12 T; 0 U; 0 Other;

Query Match 12.6%; Score 20.6; DB 6; Length 65;
 Best Local Similarity 67.4%; Pred. No. 8.1e+03;
 Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 QY 97 CGAGGCGAGTCCAGCGCTGCAAGCCACAGTGAAGAACATC 139
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 10 GGTGCACACTGAAGCTGTTGAAGACACCCAGTGAAGAACTTC 52

RESULT 25
 ADW21450/c
 ID ADW21450 standard; DNA; 75 BP.
 XX
 AC ADW21450;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE Blys binding-peptide, encoding DNA, SEQ ID 188.
 XX
 KW Blys; B lymphocyte stimulator; B lymphocyte stimulator antagonist;
 KW immune disorder; cancer; cytostatic; neoplasm; rheumatoid arthritis;
 KW multiple sclerosis; systemic lupus erythematosus; phage display;
 KW Antirheumatic; Antiarthritis; Neuroprotective; Antiinflammatory;
 KW Dermatological; Immunosuppressive; leukemia; lymphoma; myeloma; ss.
 XX
 OS Synthetic.
 XX
 PN WO2005005462-A2.
 XX
 PD 20-JAN-2005.
 XX
 PF 04-JUN-2004; 2004WO-US017682.
 XX
 PR 05-JUN-2003; 2003US-0476414P.
 PR 05-JUN-2003; 2003US-0476481P.
 PR 06-JUN-2003; 2003US-0476531P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Chan AC, Gordon NC, Kelley RF, Koehler MFT, Starovasnik MA;
 XX
 DR WPI; 2005-092059/10.
 DR P-PSDB; ADW21372.
 XX
 PT New polypeptide or Blyss antagonist, for treating an immune-related
 PT condition (e.g. rheumatoid arthritis, multiple sclerosis or systemic
 PT lupus erythematosus) or cancer (e.g. leukemia or lymphoma).
 XX
 PS Example 2; SEQ ID NO 188; 226pp; English.

CC The invention relates to a polypeptide comprising sequences of formula I,
 CC II or III, (detailed in the claims) which are antagonists of Blys (B cell
 CC stimulator). Also included are a nucleic acid molecule encoding the
 CC polypeptide, a vector comprising the nucleic acid molecule, a host cell
 CC comprising the nucleic acid molecule, a method for producing a
 CC polypeptide, a composition comprising the polypeptide optionally further
 CC comprising a physiological carrier, a method for detecting an inhibitor
 CC of Blys binding to BR3 (Blys receptor 3) in vitro, a method for
 CC inhibiting Blys binding to BR3 in a mammal, a method for inhibiting Blys
 CC signaling in a mammal and a method for treating an immune-related
 CC condition or cancer in a mammal. The sequence of Formula I, II or III is
 CC a sequence fused or conjugated to an immunoadhesion protein or to an
 CC antibody, where the antibody is a F(ab) antibody, F(ab') 2 antibody, a
 CC scfv antibody, a humanized antibody or multispecific antibody, e.g., a
 CC antibodies directed against CD20. The polypeptide is conjugated to an
 CC agent, e.g. a growth inhibitory agent, a cytotoxic agent, a detection
 CC agent, an agent that improves the bioavailability of the polypeptide and
 CC an agent that improves the half-life of the polypeptide, where the
 CC cytotoxic agent is a toxin, an antibiotic or a radioactive isotope. The
 CC polypeptide, composition and methods are useful for treating an immune-
 CC related condition (many examples given in the specification), e.g.
 CC rheumatoid arthritis, multiple sclerosis or systemic lupus erythematosus
 CC or for treating cancer (many examples given in the specification), e.g.
 CC leukemia, lymphoma or myeloma. The peptides were isolated from a phage
 CC display library, where the DNAs encoding them additionally encoded a
 CC peptide linker and an STII signal peptide. The present sequence is a DNA
 CC encoding a Blys-binding peptide of the invention.

SQ Sequence 75 BP; 12 A; 24 C; 20 G; 19 T; 0 U; 0 Other;

Query Match 12.6%; Score 20.6; DB 14; Length 75;
 Best Local Similarity 62.7%; Pred. No. 8.5e+03;
 Matches 32; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 3 TCGGCCACCTTTGATGAGGGGACTGGCCAGTTCTTAGACAGTCCCGAAGTTC 53
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 72 TCCTCCACCGGTGATGAGGTGACAGGGCACCCAGCGCGGAACCGAGAGATC 22

Search completed: March 3, 2006, 08:00:13
 Job time : 1077.86 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:29:32 ; Search time 215.424 Seconds
(without alignments)
1353.240 Million cell updates/sec

Title: US-10-655-801-3_COPY_14_177

Perfect score: 164

Sequence: 1 tctgcgcaccttgatgag.....tcaaatccagataagtgaac 164

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs; 888780828 residues

Total number of hits satisfying chosen parameters: 1395746

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents NA.*

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4: /cgn2_6/prodata/1/ina/6B COMB.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.8	13.3	78	3	US-08-928-881-22
2	21.8	13.3	78	3	US-09-543-921-22
3	21.8	13.3	78	3	US-09-491-759-22
4	20.2	12.3	78	2	US-08-089-974B-4
5	20.2	12.3	78	2	US-08-089-974B-18
6	20.2	12.3	78	2	US-08-089-974B-20
7	19.6	12.0	70	3	US-09-364-540-21
8	19.4	11.8	43	3	US-09-991-181-34
9	19.4	11.8	43	3	US-09-990-444-34
10	19.4	11.8	43	3	US-09-997-333-34
11	19.4	11.8	43	3	US-09-992-598-34
12	19.4	11.8	69	2	US-08-169-813-2
13	19.2	11.7	33	3	US-09-000-630C-6
14	19.2	11.7	33	3	US-08-862-730C-6
15	19	11.6	69	3	US-09-270-767-30297
16	18.6	11.3	47	3	US-09-422-978-377
17	18.4	11.2	47	3	US-09-422-978-14
18	18.4	11.2	3	3	US-09-443-199C-329
19	18.4	11.2	74	3	US-09-513-999C-17717
20	18.2	11.1	40	2	US-08-684-88
21	18.2	11.1	40	2	US-08-675-502-88
22	18.2	11.1	40	3	US-09-245-802-88
23	18.2	11.1	50	3	US-10-131-827-5128
24	18.2	11.1	59	3	US-09-513-999C-14163

Sequence 3, Appli	US-09-142-722-3	18	11.0	25	18
Sequence 946, App	US-09-443-199C-946	51	11.0	26	18
Sequence 1, Appli	US-08-544-087A-1	66	11.0	27	18
Sequence 18, Appli	US-09-364-540-18	70	11.0	28	18
Sequence 19, Appli	US-08-753-247-19	72	11.0	29	18
Sequence 36, Appli	US-07-795-859B-36	45	10.9	30	17.8
Sequence 36, Appli	US-08-457-616-36	45	10.9	31	17.8
Sequence 244, App	US-08-171-389-244	50	10.9	32	17.8
Sequence 244, App	US-08-123-936-244	50	10.9	33	17.8
Sequence 244, App	US-08-475-228A-244	50	10.9	34	17.8
Sequence 244, App	US-08-482-080A-244	50	10.9	35	17.8
Sequence 244, App	US-09-354-947-244	50	10.9	36	17.8
Sequence 244, App	US-09-393-346-244	50	10.9	37	17.8
Sequence 244, App	PCT-US93-12388-244	6	10.9	38	17.8
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Sequence 9, Appli	US-09-693-350-9	60	10.9	44	17.8
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Sequence 33, Appli	US-09-513-999C-29198	74	10.9	50	17.8
Sequence 18, Appli	US-09-320-424-18	77	10.9	51	17.8
Sequence 18, Appli	US-09-825-563-18	77	10.9	52	17.8
Sequence 93, Appli	US-08-253-155A-93	44	10.7	53	17.6
Sequence 22, Appli	US-08-625-209A-22	44	10.7	54	17.6
Sequence 22, Appli	US-08-853-733B-22	44	10.7	55	17.6
Sequence 1176, Ap	US-09-443-199C-1176	51	10.7	56	17.6
Sequence 28, Appli	US-08-151-574-28	56	10.7	57	17.6
Sequence 28, Appli	US-08-419-448-28	56	10.7	58	17.6
Sequence 28, Appli	US-09-233-510-28	56	10.7	59	17.6
Sequence 7, Appli	US-08-836-561-7	58	10.7	60	17.6
Sequence 8, Appli	US-09-434-123-8	64	10.7	61	17.6
Sequence 1, Appli	US-09-050-516-1	67	10.7	62	17.6
Sequence 49, Appli	US-10-278-547-1	67	10.7	63	17.6
Sequence 444, App	US-09-422-978-444	30	10.6	64	17.6
Sequence 608, App	US-09-443-199C-608	51	10.6	65	17.6
Sequence 6, Appli	US-09-621-625A-6	57	10.6	66	17.6
Sequence 113025,	US-09-396-196G-113025	25	10.5	67	17.6
Sequence 135, App	US-09-422-978-135	47	10.5	68	17.4
Patent No. 5258287	US-10-131-827-1827	50	10.5	69	17.4
Sequence 7, Appli	5258287-20	61	10.5	70	17.4
Sequence 9028, Ap	US-09-463-458A-7	72	10.5	71	17.2
Sequence 15810, A	US-09-396-196G-9028	25	10.4	72	17.2
Sequence 100928,	US-09-396-196G-100928	25	10.4	73	17.2
Sequence 100930,	US-09-396-196G-100930	25	10.4	74	17.2
Sequence 6988, Ap	US-08-584-040-6988	27	10.4	75	17.2
Sequence 974, App	US-09-671-317-974	47	10.4	76	17.2
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Sequence 1448, Ap	US-09-422-978-1448	47	10.4	78	17.2
Sequence 1879, Ap	US-09-422-978-1879	47	10.4	79	17.2
Sequence 486, App	US-10-131-827-486	50	10.4	80	17.2
Sequence 21, Appli	US-08-477-270-21	60	10.4	81	17.2
Sequence 48, Appli	US-09-586-546-48	66	10.4	82	17.2
Sequence 9, Appli	US-09-065-914B-9	66	10.4	83	17.2
Sequence 27734, A	US-09-513-999C-27734	71	10.4	84	17.2
Sequence 6996, Ap	US-09-270-767-6996	74	10.4	85	17.2
Sequence 22278, A	US-09-270-767-22278	74	10.4	86	17.2
Patent No. 5182195	5182195-3	77	10.4	87	17.2
Sequence 7348, Ap	US-09-396-196G-7348	25	10.2	88	17.2
Sequence 11869, A	US-09-371-772B-11869	38	10.2	89	17.2
Sequence 591, App	US-09-671-317-591	96	10.2	90	17.2
Sequence 1071, Ap	US-09-422-978-1071	47	10.2	91	17.2

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c	99	16.8	10.2	50	3	US-09-063-276-6	Sequence 6, Appli
c	100	16.8	10.2	50	3	US-09-324-782-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-328-881-22
; Sequence 22, Application US/08928881.
; Patent No. 6083725
; GENERAL INFORMATION:
; APPLICANT: Seiden et al., Richard F.
; TITLE OF INVENTION: THERAPY FOR ALPHA-GALACTOSIDASE A

```

,
,
,
,
,
COMPUTER READABLE FORM:
,
MEDIUM TYPE: Floppy disk
,
COMPUTER: IBM PC compatible
,
OPERATING SYSTEM: PC-DOS/MS-DOS
,
SOFTWARE: Patentin Release #1.0, Version #1.30
,
CURRENT APPLICATION DATA:
,
APPLICATION NUMBER: US/08/928,881
,

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Query Match	13.3%	Score	21.8	DB	3	Length	78
Best Local Similarity	56.2%	Pred. NO.	3.5e+02				
Matches	41	Conservative	0	Mismatches	12	Indels	0
						Gaps	0

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Qy	95	GGGGAGGCAGTGC	107	
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RESULT 2
US-09-543-921-22
; Sequence 22, Application US/09543921
; Patent No. 6395884
; GENERAL INFORMATION:
; APPLICANT: Selden et al., Richard P.
; TITLE OF INVENTION: THERAPY FOR ALPHA-GALACTOSIDASE A
; DEFICIENCY
;
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 425 Franklin Street
;

```

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,921
FILING DATE: 06-Apr-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,881
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-543-921-22

Query Match	13.3%	Score 21.8;	DB 3;	Length 78;
Best Local Similarity	56.2%;	Pred. NO. 3.5e+02;		
Matches	41;	Conservative	0;	Mismatches 32; Indels 0; Gaps 0;
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Db	5	CTACAGCTCCCGAGTCCCTGCTCTGTGCTTTTGGCTCTGCTGCTGCTGCTGCTTC	64	

Qy	95	GGGAGGCGACTGC	107
Db	65	AAGAGGCGACTGC	77

NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,759
FILING DATE: 27-Jan-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,881
FILING DATE: <Unknown>


```

? /
? HYPOTHETICAL: no
? ANTI-SENSE:
? FRAGMENT TYPE:
? ORIGINAL SOURCE:
? ORGANISM: brome mosaic virus
? STRAIN: Madison
? INDIVIDUAL ISOLATE: M1
? DEVELOPMENTAL STAGE:
? HAPOTYPE:
? TISSUE TYPE:
? CELL TYPE:
? CELL LINE:
? ORGANELLE:
? IMMEDIATE SOURCE:
? LIBRARY: no
? CLONE:
? POSITION IN GENOME:
? CHROMOSOME/SEGMENT:
? MAP POSITION: BMV RNA1
? UNITS:
? FEATURE:
? NAME/KEY: lower strand capable of forming a heteroduplex with SEQ ID 3 (het
? NAME/KEY: in Fig. 3)
? LOCATION:
? IDENTIFICATION METHOD: cdna sequencing
? OTHER INFORMATION:
? PUBLICATION INFORMATION:
? AUTHORS: Nagy, P.D.
? AUTHORS: Bujarski, J.J.
? TITLE: Targeting the site of RNA-RNA recombination in virus with antisense s
? JOURNAL: Proc. Natl. Acad. Sci. USA

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/ / AUTHORS: BUJARSKI, J.J.
 / / TITLE: Targeting the site of RNA-RNA recombination in virus with antisense s
 / / JOURNAL: Proc. Natl. Acad. Sci. USA
 / / VOLUME: 90
 / / ISSUE:
 / / PAGES: 6390-6394
 / / DATE: July 1993
 / / DOCUMENT NUMBER:
 / / FILING DATE:
 / / PUBLICATION DATE: July 1993
 / / RELEVANT RESIDUES IN SEQ ID NO: 66
 / / US-08-089-974B-4

Query Match	12.3%	Score 20.2;	DB 2;	Length 78;
Best Local Similarity	56.9%;	Pred. No. 1.4e+03;		
Matches 37;	Conservative	0;	Mismatches 28;	Indels 0;
Gaps	0;			

Qy 87 CTTATCCCGGGGAGGCGAGTGCAGCCAGCTCGAAGCCCCACAGTGAAGAACTCTGAGCTC 146

Db 75 CTCTCTCGAGCAGAGGTCTCACACAGAGACAAGCGCATCACTTAAACAATTAAGATC 16

Qy	147 AAATC 151
Db	15 AAATC 11

RESULT 5

RESOUR 3
US-08-089-974B-18/c
; Sequence 18, Application US/08089974B
: Patent No. 5877401

Patent No.: 3677401
GENERAL INFORMATION:
APPLICANT: Bujarski, Jozef J.
APPLICANT: Nagy, Peter D.
TITLE OF INVENTION: Targeting and Enhancing RNA-RNA Recombination
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:

ADDRESS: Grace J. Fishel
STREET: 929 Fee Fee, Suite 100
CITY: St. Louis, MO
STATE: Missouri
COUNTRY: USA
ZIP: 63043

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LOCATION: BMV RNA1/BMV RNA3
IDENTIFICATION METHOD: cDNA sequencing
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Nagy, P.D.
AUTHORS: Bujarski, J.J.
TITLE: Targeting the site of RNA-RNA recombination in virus with antisense s
JOURNAL: Proc. Natl. Acad. Sci. USA
VOLUME: 90
ISSUE:
PAGES: 6390-6394
DATE: July 1993
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE: July 1993
RELEVANT RESIDUES IN SEQ ID NO: 67

US-08-089-974B-20

Query Match 12.3%; Score 20.2; DB 2; Length 78;
Best Local Similarity 56.9%; Pred. No. 1.4e+03;
Matches 37; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 87 CTTACCCCGGAGGAGGCTGACCCAGCTGCAAGCCCAAGTGAAGAACATCTGAGCTC 146
Db 75 CTCCTCTGAGCAGAGGCTCTCACACAGACAGAGCCGATCATCTTACACAAATTAAGATC 16

QY 147 AAATC 151
Db 15 AAATC 11

RESULT 7

US-09-364-540-21/c
Sequence 21, Application US/09364540A

Patent No. 6762290

GENERAL INFORMATION:

APPLICANT: Janjic, Nebojsa

APPLICANT: Gold, Lairy

TITLE OF INVENTION: High Affinity Vascular Endothelial Growth Factor (VEGF)

TITLE OF INVENTION: Receptor Nucleic Acid Ligands and Inhibitors

FILE REFERENCE: NEX88

CURRENT APPLICATION NUMBER: US/09/364,540A

CURRENT FILING DATE: 1999-07-29

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 21

LENGTH: 70

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: modified base

LOCATION: (1)..(70)

OTHER INFORMATION: All pyrimidines are 2'F.

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Sequence

US-09-364-540-21

Query Match

Best Local Similarity 12.0%; Score 19.6; DB 3; Length 70;

Matches 31; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 18 GAGGAGCACTGGCGAGTCTTAGACAGTCGCCAAGTTCTCAAGGCACAGGTC 67
Db 64 GAGTGTCTGACAGGAGCAGCAAAATACGAAGTTCCAAAGGAGCACCTC 15

RESULT 8

US-09-991-181-34

Sequence 34, Application US/09991181

Patent No. 6913919

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Auscin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS ENCODING THE SAME
FILE REFERENCE: P2730PICS3
CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR APPLICATION NUMBER: 60/087607
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472

APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
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PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
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PRIOR FILING DATE: 1998-06-10
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PRIOR FILING DATE: 1998-06-11
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PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
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PRIOR FILING DATE: 1998-06-19
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;; PRIOR APPLICATION NUMBER: 60/090694
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;; PRIOR APPLICATION NUMBER: 60/090695
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;; PRIOR APPLICATION NUMBER: 60/090696
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;; PRIOR FILING DATE: 1998-06-26
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;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091798
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 11.8%; Score 19.4; DB 3; Length 43;
Best Local Similarity 70.3%; Pred. No. 2e+03;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 79 TGACTGCTCTTACCCGGGAGGACGTGGCAGCCAGCT 115
DB 1 TGACTGCACTTACCCCTGGCAAGCTGTGAGCCAGCT 37

RESULT 12
US-08-169-813-2
; Sequence 2, Application US/08169813
; Patent No. 5591823
; GENERAL INFORMATION:
; APPLICANT: Hung, Paul P.
; APPLICANT: Lee, Shaw-Guang L.
; APPLICANT: Kalyan, Narendra K.
; TITLE OF INVENTION: EXPRESSION OF SPECIFIC IMMUNOGENS
; TITLE OF INVENTION: USING VIRAL ANTIGENS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5, inch, 360 kb storage
; COMPUTER: Emerson 16MHz
; OPERATING SYSTEM: DOS 3.3
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/169,813
; FILING DATE: 17-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/805,105
; FILING DATE: 11-Dec-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert Schaffer, Esq.
; REGISTRATION NUMBER: 31,194
; REFERENCE/DOCKET NUMBER: 0632/06916

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 527-7700
;; TELEFAX: (212) 753-6237
;; TELEX: 236687
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 69 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double stranded
;; TOPOLOGY: unknown
;; FEATURE:
;; OTHER INFORMATION: Anti-sense strand begins four
;; OTHER INFORMATION: bases before the sense strand,
;; OTHER INFORMATION: adding the sequence CCGG and
;; OTHER INFORMATION: ends four bases before the
;; OTHER INFORMATION: sense strand.
US-08-169-813-2

Query Match 11.8%; Score 19.4; DB 2; Length 69;
Best Local Similarity 60.4%; Pred. No. 2.5e+03;
Matches 32; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 30 CAGTTCTACAGAGTCCGGAAGTTCTCAAGGCACAGTCTCTTCTGTTGAC 82
DB 3 CAGTACTACAGCCCGCAAAACCAAGGATTCATTGTATTCTCAC 55

RESULT 13
US-09-000-630C-6
; Sequence 6, Application US/09000630C
; Patent No. 6018029
; GENERAL INFORMATION:
; APPLICANT: Fuller, Gerald M.
; APPLICANT: Fuentes, Nelson L.
; TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
; TITLE OF INVENTION: Antagonist
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White
; STREET: 2001 Park Place, Suite 1400
; CITY: Birmingham
; STATE: Alabama
; COUNTRY: USA
; ZIP: 35203-2736
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch,
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Microsoft Windows
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/000,630C
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/862,730
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
US-09-000-630C-6

Query Match 11.7%; Score 19.2; DB 3; Length 33;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 91 CCCCGGGAGGAGTGGCAGCCAGCTGCAAGCC 122
DB 2 CCTCTGGGAGAAATCCAGCAAGATGCAAGCC 33

	Query Match	11.2%	Score 18.4;	DB 3;	Length 51;
	Best Local Similarity	63.4%;	Pred. No. 5.1e+03;		
	Matches 25;	Conservative 0;	Mismatches 11;	Indels 0;	Gaps 0;
QY	63	AGGTCCTCTTCTGGTTTGACTGCTCTTACCCCGGGG	98		
Db	48	AGGTCCTATTCTGGTTGCTCAGTCCCAACCTCGG	13		

Query Match	11.2%	Score 18.4;	DB 3;	Length 74;
Best Local Similarity	54.4%;	Prod. NO. 6e+03;		
Matches 37;	Conservative 0;	Mismatches 31;	Indels 0;	Gaps 0;

60	CACAGGTCTCTTCGTGTTTTGACTGTCCTTATCCCGGGGAGGACGTGCGACGCTGCAA	119
QY		
7	CACAACTAAATCTCTGTGCTCAGCTCCGAGTAGCTGGGAGTATTAAGCGCCACACAGCAT	66
Db		

DB 67 GCCCAACA 74

01 00000000 01

RESULT 20
US-08-425-684-88
Sequence 88, Application US/08425684
Patent No. 5834252
GENERAL INFORMATION:
APPLICANT: STEMMER PH.D., WILLEM P.C.
TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
NUMBER OF SEQUENCES: 136
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND CREW
STREET: ONE MARKET PLAZA, STEUART STREET TOWER, 20TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,684
FILING DATE: 18-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DUNN ESQ., TRACY J.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 16528J-015400US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
US-08-425-684-88

Query Match 11.1%; Score 18.2; DB 2; Length 40;
Best Local Similarity 74.2%; Pred. No. 5.4e+03;
Matches 23; Conservative 0; Mismatches 8; Indels

Qy 124 CACAGTGAAGAACAATCTGAGCTCAAATCCAG 154
| | | | | | | | | | | | | |
Db 10 CGCAGGAAGAACAATGTGAGCAAAAGGCCAG 40

RESULT 21
US-08-675-502-88
; Sequence 88, Application US/08675502
; Patent No. 5928905
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; APPLICANT: LIPSHUTE, ROBERT J.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675.502
; FILING DATE: 03-JUL-1996

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,684
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05480
; FILING DATE: 18-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY, ESO., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 16528J-015410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; US-08-675-502-88
;
Query Match 11.1%; Score 18.2; DB 2; Length 40;
Best Local Similarity 74.2%; Pred. No. 5.4e+03;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 124 CACAGTCAGAGACATCTGAGCTCAATCCAG 154
Db 10 CGCAGGAAGAACAATGTGAGCAAAAGGCCAG 40

RESULT 22
US-09-245-802-88
; Sequence 88, Application US/09245802
; Patent No. 6489146
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; APPLICANT: LIPSHUTZ, ROBERT J.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/245,802
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05480
; FILING DATE: 18-APR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY, ESO., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 16528J-015410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422

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US-09-513-999C-14163

Query Match 11.1%; Score 18.2; DB 3; Length 59;
 Best Local Similarity 58.2%; Pred. No. 6.4e+03;
 Matches 32; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 QY 85 TCCTTACCCGGGAGCGAGTGCAGCCAGCTGCAAGCCCCACAGTGAAGACATC 139
 Db 57 TCGTCCCTCACTCGCGCGCGCGCGCTGCTTAGGACACAAAAGGACATC 3

RESULT 25

US-09-142-722-3
 ; Sequence 3, Application US/09142722
 ; Patent No. 6605447
 ; GENERAL INFORMATION:
 ; APPLICANT: Weiss, Robert M.
 ; APPLICANT: Sessa, William C.
 ; APPLICANT: Wheeler, Marcia A.
 ; APPLICANT: Smith, Shannon D.
 ; APPLICANT: YALE UNIVERSITY
 ; TITLE OF INVENTION: Methods and Means of Detecting Nitric Oxide
 ; FILE REFERENCE: YAL-0024
 ; CURRENT APPLICATION NUMBER: US/09/142,722
 ; CURRENT FILING DATE: 1998-09-14
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-142-722-3

Query Match 11.0%; Score 18; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CACCTTTGATGAGGGGAC 25
 Db 1 CACCTTTGATGAGGGGAC 18

Search completed: March 3, 2006, 07:34:51
 Job time : 216.424 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:34:36 ; Search time 221.11 Seconds
(without alignments)
673.188 Million cell updates/sec

Title: US-10-655-801-21

Perfect score: 18

Sequence: 1 tgccttgagaacttcggg 18

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Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

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Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	9	US-10-182-049-21
2	14.8	82.2	25	10	US-11-036-317-592184
3	14.8	82.2	25	10	US-11-036-317-812924
4	14.8	82.2	25	10	US-11-060-756-162369
5	14.4	80.0	25	7	US-10-719-956-352445
6	14.4	80.0	25	10	US-11-036-317-142883
7	14	77.8	25	8	US-10-719-900-511931
8	14	77.8	25	8	US-10-719-900-581095
9	13.8	76.7	20	7	US-10-380-126-36
10	13.8	76.7	20	5	US-10-098-263B-93346
11	13.8	76.7	25	7	US-10-719-956-542451
12	13.8	76.7	25	7	US-10-719-956-684475
13	13.8	76.7	25	10	US-11-036-317-43312
14	13.8	76.7	25	10	US-11-036-317-65279
15	13.4	74.4	25	7	US-10-719-956-207934
16	13.4	74.4	25	7	US-10-719-956-254482
17	13.4	74.4	25	7	US-10-719-956-306955
18	13.4	74.4	25	7	US-10-719-956-418803
19	13.4	74.4	25	7	US-10-719-956-429526
20	13.4	74.4	25	7	US-10-719-956-442037
21	13.4	74.4	25	8	US-10-719-900-346702
22	13.4	74.4	25	8	US-10-719-900-833460
23	13.4	74.4	25	8	US-10-719-900-878385

Sequence 440654,
Sequence 701048,
Sequence 748820,
Sequence 282, App
Sequence 8979, Ap
Sequence 2, Appl
Sequence 45113, A
Sequence 244426,
Sequence 280310,
Sequence 398900,
Sequence 406389,
Sequence 468942,
Sequence 659705,
Sequence 43968,
Sequence 521447,
Sequence 959400,
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Sequence 978806,
Sequence 1069, Ap
Sequence 5488, A
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Sequence 106398,
Sequence 434343,
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Sequence 702596,
Sequence 812925,
Sequence 30, Appl
Sequence 25193, A
Sequence 8222, Ap
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Sequence 107068,
Sequence 235531,
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Sequence 419259,
Sequence 434919,
Sequence 462939,
Sequence 861174,
Sequence 153736,
Sequence 153735,
Sequence 182816,
Sequence 182817,
Sequence 196898,
Sequence 196899,
Sequence 30, Appl

97 12.4 68.9 21 8 US-10-751-736-53330 Sequence 53330, A
98 12.4 68.9 22 3 US-09-998-547-5 Sequence 5, Appli
99 12.4 68.9 22 8 US-10-819-714-5 Sequence 5, Appli
100 12.4 68.9 25 7 US-10-717-597-2349 Sequence 2349, Ap

ALIGNMENTS

RESULT 1
US-10-182-049-21
; Sequence 21, Application US/10182049
; Publication No. US2005011322A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSION
; FILE REFERENCE: RTSP-0360
; CURRENT APPLICATION NUMBER: US/10/182,049
; CURRENT FILING DATE: 2002-07-27
; PRIOR APPLICATION NUMBER: 09/490,208
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-182-049-21

Query Match 100.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TGCCTTGAGAACTTCGGG 18
Db 1 TGCCTTGAGAACTTCGGG 18
RESULT 2
US-11-036-317-592184/c
; Sequence 592184, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 592184
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-592184

Query Match 82.2%; Score 14.8; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 TGCCTTGAGAACTTCGGG 18
Db 19 TGCCTTGAGGAATTCGGG 2

RESULT 3

US-11-036-317-812924
; Sequence 812924, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 812924
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-812924

Query Match 82.2%; Score 14.8; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 TGCCTTGAGAACTTCGGG 18
Db 6 TGCCTTGAGAACTTCGGG 23

RESULT 4
US-11-060-756-162369/c
; Sequence 162369, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 162369
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-162369

Query Match 82.2%; Score 14.8; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 TGCCTTGAGAACTTCGGG 18
Db 24 TGCCTTGAGAACTTCGGG 7

RESULT 5
US-10-719-956-352445/c
; Sequence 352445, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 352445


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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-352445

Query Match      80.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 8e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 3 CCTTGAGAACTTCGGG 18
   |||||
Db 22 CCTTGAGAACTTCGGG 7

RESULT 6
US-11-036-317-142883/c
; Sequence 142883, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 142883
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-142883

Query Match      80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 8e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 3 CCTTGAGAACTTCGGG 18
   |||||
Db 25 CCTTGAGAACTTCGGG 10

RESULT 7
US-10-719-900-511931
; Sequence 511931, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse.
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 511931
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-511931

Query Match      77.8%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTT 14
   |||||
Db 9 TGCCTTGAGAACTT 22

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RESULT 8
US-10-719-900-581095/c
; Sequence 581095, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 581095
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-581095

Query Match      77.8%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTTGAGAACTTCGG 17
   |||||
Db 24 CTTGAGAACTTCGG 11

RESULT 9
US-10-380-126-36/c
; Sequence 36, Application US/10380126
; Publication No. US20040029824A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-1 EXPRESSION
; FILE REFERENCE: RTSP-0175
; CURRENT APPLICATION NUMBER: US/10/380,126
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 09/657,042
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-126-36

Query Match      76.7%; Score 13.8; DB 7; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTCGG 18
   |||||
Db 18 GCCTTGAGAACTTCAGG 2

RESULT 10
US-10-098-263B-93346/c
; Sequence 93346, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16

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; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 207934
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-207934

Query Match 74.4%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCCTTGAGAACTTC 15
Db 2 TTCCTTGAGAACTTC 16

RESULT 16

US-10-719-956-254482
; Sequence 254482, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 254482
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-254482

Query Match 74.4%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCTTGAGAACTTCG 17
Db 1 CCTTGAGAACTTCG 15

RESULT 17

US-10-719-956-306955/c
; Sequence 306955, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 306955
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-306955

Query Match 74.4%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCCTTGAGAACTTC 15
||| |||||

Db 15 TGCATTGAGAACTTC 1

RESULT 18

US-10-719-956-418803/c
; Sequence 418803, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 418803
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-418803

Query Match 74.4%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCCTTGAGAACTTC 15
Db 16 TGCCCTTGAGAACTTC 2

RESULT 19

US-10-719-956-429526/c
; Sequence 429526, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 429526
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-429526

Query Match 74.4%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCCTTGAGAACTTC 15
Db 16 TGCCCTTGAGAACTTC 2

RESULT 20

US-10-719-956-442037
; Sequence 442037, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 442037
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-442037

Query Match 74.4%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GCCTTGAGAACTTCG 16
Db 2 GCCTTGAGAACTTAG 16
|||||

RESULT 21
US-10-719-900-346702/c
; Sequence 346702, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 346702
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-346702

Query Match 74.4%; Score 13.4; DB 8; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 CTTGAGAACTTCGGG 18
Db 15 CTTAGAACTTCGGG 1
|||||

RESULT 22
US-10-719-900-833460
; Sequence 833460, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 833460
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-833460

Query Match 74.4%; Score 13.4; DB 8; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGCCTTGAGAACTTC 15
Db 3 TGCCTTGAGAACTTC 17
|||||

RESULT 23
US-10-719-900-878385/c
; Sequence 878385, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 878385
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-878385

Query Match 74.4%; Score 13.4; DB 8; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGCCTTGAGAACTTC 15
Db 17 TGCCTTGAGAACTTC 3
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RESULT 24
US-11-036-317-440654/c
; Sequence 440654, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 440654
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-440654

Query Match 74.4%; Score 13.4; DB 10; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 CTTGAGAACTTCGGG 18
Db 21 CTTGAGAACTTCGGG 7
|||||

RESULT 25
US-11-036-317-701048/c
; Sequence 701048, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639

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; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 701048
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-701048

Query Match      74.4%; Score 13.4; DB 10; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 TGCCTTGAGAACTTC 15
        |||||
Db      25 TGCCTTGAGAGCTTC 11

Search completed: March 3, 2006, 08:48:49
Job time : 223.11 secs

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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:35:12 ; Search time 97.8559 Seconds
(without alignments)
403.294 Million cell updates/sec

Title: US-10-655-801-21

Perfect score: 18
Sequence: 1 tgccttgagaactcggg 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 11869656

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications NA_New.*

- 1: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq.*
- 2: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/prodata/1/pubpna/US05_NEW_PUB.seq.*
- 6: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq.*
- 7: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq.*
- 8: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq.*
- 9: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
- 12: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
- 13: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	77.8	19	US-11-101-244-1087177	Sequence 1087177
2	14	77.8	19	US-11-083-784-1087177	Sequence 1087177
3	13.8	76.7	21	US-10-310-914A-249584	Sequence 249584
4	13.8	76.7	25	US-11-121-849-233627	Sequence 233627
5	13.8	76.7	25	US-11-121-849-310353	Sequence 310353
6	13.8	76.7	61	US-10-310-914A-4446	Sequence 4446, Ap
7	13.8	76.7	63	US-10-310-914A-12044	Sequence 12044, A
8	13.8	76.7	78	US-10-310-914A-7665	Sequence 7665, Ap
9	13.4	74.4	19	US-11-101-244-644548	Sequence 644548
10	13.4	74.4	19	US-11-101-244-1499872	Sequence 1499872
11	13.4	74.4	19	US-11-101-244-1506108	Sequence 1506108
12	13.4	74.4	19	US-11-083-784-644548	Sequence 644548
13	13.4	74.4	19	US-11-083-784-1499872	Sequence 1499872
14	13.4	74.4	19	US-11-083-784-1506108	Sequence 1506108
15	13.4	74.4	30	US-10-857-780-3518	Sequence 3518, Ap
16	13.2	73.3	22	US-10-310-914A-1205266	Sequence 1205266
17	13.2	73.3	24	US-10-310-914A-346426	Sequence 346426
18	13.2	73.3	25	US-11-121-849-27119	Sequence 27119, A
19	13.2	73.3	25	US-11-121-849-235259	Sequence 235259
20	13.2	73.3	25	US-11-121-849-289504	Sequence 289504

25	12	73.3	US-11-121-849-346138	Sequence 346138
25	12	73.3	US-11-121-849-448511	Sequence 448511
25	12	73.3	US-11-121-849-448519	Sequence 448519
25	12	73.3	US-11-121-849-448520	Sequence 448520
25	12	73.3	US-11-121-849-448521	Sequence 448521
25	12	73.3	US-11-136-527-78322	Sequence 78322, A
25	12	73.3	US-11-136-527-78325	Sequence 78325, A
26	8	73.3	US-10-310-914A-1205217	Sequence 1205217
29	19	72.2	US-11-101-244-1498131	Sequence 1498131
30	13	72.2	US-11-101-244-1498154	Sequence 1498154
31	13	72.2	US-11-083-784-1498131	Sequence 1498131
32	13	72.2	US-11-083-784-1498154	Sequence 1498154
33	13	72.2	US-11-121-849-320432	Sequence 320432
34	13	72.2	US-11-101-244-98914	Sequence 427246
35	12	71.1	US-11-101-244-280446	Sequence 98914, A
36	12	71.1	US-11-101-244-1308527	Sequence 1308527
37	12	71.1	US-11-083-784-98914	Sequence 1308527
38	12	71.1	US-11-083-784-280446	Sequence 280446
39	12	71.1	US-11-083-784-1308527	Sequence 1308527
40	12	71.1	US-10-310-914A-540641	Sequence 540641
41	12	71.1	US-10-310-914A-870473	Sequence 870473
42	8	71.1	US-10-310-914A-1359780	Sequence 1359780
43	12	71.1	US-11-121-849-33481	Sequence 33481, A
44	12	71.1	US-11-121-849-233628	Sequence 233628
45	12	71.1	US-11-121-849-241966	Sequence 241966
46	12	71.1	US-11-121-849-351354	Sequence 351354
47	12	71.1	US-11-136-527-12129	Sequence 12129, A
48	12	71.1	US-11-136-527-12163	Sequence 12163, A
49	12	71.1	US-11-136-527-78345	Sequence 78345, A
50	12	71.1	US-11-136-527-180264	Sequence 180264
51	12	71.1	US-11-136-527-201986	Sequence 201986
52	12	71.1	US-11-136-527-377987	Sequence 377987
53	12	71.1	US-11-136-527-345431	Sequence 345431
54	12	71.1	US-11-136-527-345441	Sequence 345441
55	12	71.1	US-11-175-859-22295	Sequence 22295, A
56	12	71.1	US-11-175-859-61257	Sequence 61257, A
57	12	71.1	US-11-175-859-66639	Sequence 66639, A
58	12	70.0	US-10-310-914A-1179854	Sequence 1179854
59	12	68.9	US-10-310-914A-695252	Sequence 695252
60	12	68.9	US-11-101-244-380230	Sequence 380230
61	12	68.9	US-11-101-244-500898	Sequence 500898
62	12	68.9	US-11-101-244-622204	Sequence 622204
63	12	68.9	US-11-101-244-654979	Sequence 654979
64	12	68.9	US-11-101-244-783862	Sequence 783862
65	12	68.9	US-11-101-244-800303	Sequence 800303
66	12	68.9	US-11-101-244-818742	Sequence 818742
67	12	68.9	US-11-101-244-833455	Sequence 833455
68	12	68.9	US-11-101-244-858952	Sequence 858952
69	12	68.9	US-11-101-244-1056312	Sequence 1056312
70	12	68.9	US-11-101-244-1590389	Sequence 1590389
71	12	68.9	US-11-083-784-380230	Sequence 380230
72	12	68.9	US-11-083-784-500898	Sequence 500898
73	12	68.9	US-11-083-784-622204	Sequence 622204
74	12	68.9	US-11-083-784-654979	Sequence 654979
75	12	68.9	US-11-083-784-783862	Sequence 783862
76	12	68.9	US-11-083-784-800303	Sequence 800303
77	12	68.9	US-11-083-784-818742	Sequence 818742
78	12	68.9	US-11-083-784-833455	Sequence 833455
79	12	68.9	US-11-083-784-858952	Sequence 858952
80	12	68.9	US-11-083-784-1056312	Sequence 1056312
81	12	68.9	US-11-083-784-1590389	Sequence 1590389
82	12	68.9	US-10-310-914A-695253	Sequence 695253
83	12	68.9	US-10-971-559-5	Sequence 5, Appli
84	12	68.9	US-10-310-914A-141070	Sequence 141070
85	12	68.9	US-11-121-849-108174	Sequence 108174
86	12	68.9	US-11-121-849-142768	Sequence 142768
87	12	68.9	US-11-121-849-23258	Sequence 23258
88	12	68.9	US-11-121-849-302576	Sequence 302576
89	12	68.9	US-11-121-849-354517	Sequence 354517
90	12	68.9	US-11-121-849-471385	Sequence 471385
91	12	68.9	US-11-121-849-471386	Sequence 471386
92	12	68.9	US-11-121-849-471387	Sequence 471387
93	12	68.9	US-11-121-849-471387	Sequence 471387

Sequence 471388,
Sequence 471389,
Sequence 471390,
Sequence 608376,
Sequence 50275, A
Sequence 50276, A
Sequence 50283, A

94 12.4 68.9 25 12 US-11-121-849-471388
95 12.4 68.9 25 12 US-11-121-849-471389
96 12.4 68.9 25 12 US-11-121-849-471390
97 12.4 68.9 25 12 US-11-121-849-608376
98 12.4 68.9 25 12 US-11-136-527-50275
99 12.4 68.9 25 12 US-11-136-527-50276
100 12.4 68.9 25 12 US-11-136-527-50283

ALIGNMENTS

RESULT 1

US-11-101-244-1087177
; Sequence 1087177, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1087177
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1087177

Query Match 77.8%; Score 14; DB 10; Length 19;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTC 15
DB 1 GCCUUGAGAACUUC 14
||||:|||||

RESULT 2

US-11-083-784-1087177
; Sequence 1087177, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1087177
; LENGTH: 19

; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1087177

Query Match 77.8%; Score 14; DB 11; Length 19;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTC 15
DB 1 GCCUUGAGAACUUC 14
||||:|||||

RESULT 3

US-10-310-914A-249584/c
; Sequence 249584, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 249584
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-249584

Query Match 76.7%; Score 13.8; DB 8; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGG 17
DB 17 TGCCTTGAGAAATTCG 1
|||||

RESULT 4

US-11-121-849-233627
; Sequence 233627, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Sa
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 233627
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-233627

Query Match 76.7%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTCGG 18
DB 3 GCCTTGAGAACTTCGG 19
|||||

RESULT 5


```

; LENGTH: 63
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-12044

Query Match 76.7% Score 13.8; DB 8; Length 63;
Best Local Similarity 88.2%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 2 GCCTTGAGAACTTCGGG 18
   |||||
Db 23 GCTTTCAGAACATCGGG 7

RESULT 8
US-10-310-914A-7665
; Sequence 7665, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory
; FILE REFERENCES: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7665
; LENGTH: 78
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-7665

Query Match 76.7% Score 13.8; DB 8; Length 78;
Best Local Similarity 70.6%; Pred. No. 2.2e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0

QY 2 GCCTTGAGAACTTCGGG 18
   |||||
Db 7 GCCUGGACACUUCGGG 23

RESULT 9
US-11-101-244-644548/c
; Sequence 644548, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCES: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 644548
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-644548

Query Match 74.4% Score 13.4; DB 10; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0

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QY 3 CCTTGAGAACTTCGG 17
|||||
Db 15 CCTTGAGCACTTCGG 1

RESULT 10

US-11-101-244-1499872/c
; Sequence 1499872, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1499872
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1499872

Query Match 74.4%; Score 13.4; DB 10; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTC 15
|||||
Db 17 TGCCTTGAGAGCTTC 3

RESULT 11

US-11-101-244-1506108/c
; Sequence 1506108, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1506108
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1506108

Query Match 74.4%; Score 13.4; DB 10; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCTTGAGAACTTCGG 17
|||||
Db 18 CCTTGAGAACTTCGG 4

RESULT 12

US-11-083-784-644548/c
; Sequence 644548, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 644548
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-644548

Query Match 74.4%; Score 13.4; DB 11; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCTTGAGAACTTCGG 17
|||||
Db 15 CCTTGAGCACTTCGG 1

RESULT 13

US-11-083-784-1499872/c
; Sequence 1499872, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1499872
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1499872

Query Match 74.4%; Score 13.4; DB 11; Length 19;

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Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTC 15
    |||||
Db 17 TGCCTTGAGAGCTTC 3

RESULT 14
US-11-083-784-1506108/c
; Sequence 1506108, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1506108
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1506108

Query Match 74.4%; Score 13.4; DB 11; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCTTGAGAACTTCGG 17
    |||||
Db 18 CCTTAAGAACTTCGG 4

RESULT 15
US-10-857-780-3518
; Sequence 3518, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAWMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: RENELAND, RIKARD HENRY
; APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/857,780
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3518
; LENGTH: 30
; TYPE: DNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-10-857-780-3518

Query Match 74.4%; Score 13.4; DB 8; Length 30;
Best Local Similarity 93.3%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTC 15
    |||||
Db 9 TGCCTTGAGAACTTC 23

RESULT 16
US-10-310-914A-1205266/c
; Sequence 1205266, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1205266
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1205266

Query Match 73.3%; Score 13.2; DB 8; Length 22;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18
    |||||
Db 21 TGCCTTCAGAACTTCAGG 4

RESULT 17
US-10-310-914A-346426/c
; Sequence 346426, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 346426
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-346426

Query Match 73.3%; Score 13.2; DB 8; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18
    |||||
Db 21 TGCCTTGAGAGCTTCGGT 4

RESULT 18

```

```

US-11-121-849-27119
; Sequence 27119, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 27119
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-27119

Query Match      73.3%; Score 13.2; DB 12; Length 25;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTTCGG 18
    | | | | | | | | | |
Db 4 TCCCGTGAGAACTTCGG 21

RESULT 19
US-11-121-849-235259
; Sequence 235259, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 235259
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-235259

Query Match      73.3%; Score 13.2; DB 12; Length 25;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTTCGG 18
    | | | | | | | | | |
Db 4 TGCCTTGAGAACTTCGG 21

RESULT 20
US-11-121-849-289504/c
; Sequence 289504, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904

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Db 19 TGCCTTGAGGAACCTCGG 2

RESULT 23

US-11-121-849-448519/c
; Sequence 448519, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 448519
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-448519

Query Match 73.3%; Score 13.2; DB 12; Length 25;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGGAACCTCGG 18

Db 23 TGCCTTGAGGAACCTCGG 6

RESULT 24

US-11-121-849-448520/c
; Sequence 448520, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 448520
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-448520

Query Match 73.3%; Score 13.2; DB 12; Length 25;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGGAACCTCGG 18

Db 21 TGCCTTGAGGAACCTCGG 4

RESULT 25

US-11-121-849-448521/c
; Sequence 448521, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849

; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 448521
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-448521

Query Match 73.3%; Score 13.2; DB 12; Length 25;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGGAACCTCGG 18

Db 19 TGCCTTGAGGAACCTCGG 2

Search completed: March 3, 2006, 07:56:43
Job time : 98.0559 secs

This Page Blank (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:25:53 ; Search time 8972.05 Seconds
(without alignments)
855.220 Million cell updates/sec

Title: US-10-655-801-3_COPY_14_177
Perfect score: 164
Sequence: 1 tctcgccaccttgatgag.....tcaaatccagataagtaca 164

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 512758

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_hc:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_gss1:
10: gb_gss2:
11: gb_gss3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	23.2	14.1	50	7	CF981901 maj75a12
C 2	23.2	14.1	58	10	CL639648
C 3	21.6	13.2	71	9	AZ791987 P208B09 G
C 4	21.2	12.9	72	7	CV305418 t162a05.b
C 5	21.2	12.9	72	7	CV305419 t162a05.g
C 6	20.8	12.7	66	3	BJ083039 BJ083039
C 7	20.8	12.7	75	8	H84929 YV85h01.e1
C 8	20.6	12.6	67	9	AZ768319 IM0568E17
C 9	20.6	12.6	74	10	CL603643
C 10	20.6	12.6	80	11	DQ051485
C 11	20.4	12.4	60	9	AZ829920 2M0107A19
C 12	20.4	12.4	79	1	AA917946 ol16804.8
C 13	20.2	12.3	57	10	CG869849 XS0340 Sa
C 14	20.2	12.3	77	4	AK198748 Mus muscu
C 15	20.2	12.3	77	4	AK198748 Mus muscu
C 16	20.2	12.3	77	4	AK198748 Mus muscu
C 17	19.8	12.1	64	9	AF149527 AF149527
C 18	19.8	12.1	77	9	AZ615721 IM0445N01
C 19	19.8	12.1	80	10	AG829487 Sus scrofa
C 20	19.8	12.1	80	10	CL869085 abes4c01.
C 21	19.6	12.0	47	9	BH806710 100807580
C 22	19.6	12.0	74	10	CG712884 1119029E0

AG217126 Drosophila	78	10	AG217126
AL462137 T. brucei	59	11	TA112C05Q
CG638372 OST367812	62	10	CG638372
CG136144 104.521.1	68	10	CG136144
BE043135 hK48D02.y	63	2	BE043135
CG479308 OST10037	68	10	CG479308
CG564040 OST187822	72	10	CG564040
AI650549 wa92D01.x	80	1	AI650549
CO745478 TGESt2yp0	71	7	CO745478
CG119567 104.496.1	79	10	CG119567
DR033729 5000G1E10	80	8	DR033729
BZ664011 SALK.0276	67	9	BZ664011
CG557728 OST174378	67	10	CG557728
CZ4767204 d08233-5p	70	10	CZ4767204
BU647204 1112056E0	77	5	BU647204
DR083206 PMU51-016	77	8	DR083206
DN337550 LJB3187-0	79	8	DN337550
CZ906313 BC0210 Sa	56	10	CZ906313
AI536756 t01803.x	61	1	AI536756
AI795111 sb7609.y	64	1	AI795111
BQ100258 ph74606.y	73	3	BQ100258
CB832486 SWbmfCAV	73	6	CB832486
AL195007 Tetraodon	73	10	CNS02FGM
CA587101 LBG27046	53	6	CA587101
AI582356 t667005.x	64	1	AI582356
AI094171 q829A09.8	70	1	AI094171
AI554288 tq05d02.x	73	1	AI554288
CL303202 F019A02 G	43	1	AA227334
CG729734 1119114D0	74	10	CG729734
AA017154 z841c01.8	76	1	AA017154
BQ269183 ik22c02.y	78	3	BQ269183
CL213371 A046E05 G	79	10	CL213371
AA097244 mm35b10.x	80	1	AA097244
CN922421 000410AEL	51	7	CN922421
BZ354994 SALK.1262	60	9	BZ354994
AL797821 AL797821	61	1	AL797821
AI569396 tm86408.x	64	1	AI569396
CG638918 OST369134	66	10	CG638918
DQ041915 Homo sapi	68	11	DQ041915
DQ041916 Pan trogl	68	11	DQ041916
BX690564 BX690564	5	5	BX690564
DR108645 JHU168E11	69	8	DR108645
CV307374 tJ43d06.b	77	7	CV307374
CC325376 TEA231 Ba	77	9	CC325376
AA490024 ab02b06.8	79	1	AA490024
CC883422 SALK.0942	45	9	CC883422
CA586216 LBC01186	49	6	CA586216
CA587090 LBG27p33	49	6	CA587090
AZ817412 2M0086J11	57	9	AZ817412
AI318464 fa80h04.x	60	1	AI318464
CG631433 OST347814	61	10	CG631433
AZ767834 IM0567023	62	9	AZ767834
CR064445 Forward 8	62	11	CR064445
AA706076 ah25h02.8	65	1	AA706076
BH000484 2M0288D24	66	9	BH000484
CZ483689 F01213-5p	67	10	CZ483689
CZ488696 f06057-5p	67	10	CZ488696
BX189635 Danilo rer	68	10	BX189635
BX128997 Danilo rer	69	10	BX128997
BJ036111 BJ036111	70	3	BJ036111
AI826111 WK28901.x	71	1	AI826111
BH217655 1006057D1	71	9	BH217655
CR085416 Reverse 8	71	11	CR085416
CG526501 OST103143	72	10	CG526501
CK725806 SWbL3CAW	73	7	CK725806
AA136590 zn95c03.8	74	1	AA136590
CG869661 XR0120 Sa	75	10	CG869661
H74365 269 Deletio	78	8	H74365
H42857 yo10e01.e1	79	8	H42857

96 18.2 11.1 80 10 CZ471354
 97 18.2 11.1 80 11 DE059536
 98 11.0 48 10 CZ459338
 99 11.0 50 10 CZ475687
 100 11.0 52 9 AZ584594
 c 100 11.0 52 9 AZ584594

ALIGNMENTS

RESULT 1
 CF981901/c
 LOCUS
 DEFINITION
 musculus CDNA clone IMAGE:7031702 5', mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

CF981901 50 bp mRNA linear EST 18-DEC-2003
 maj75a12-y1 McCarrey Eddy 18 day preleptotene spermatocytes Mus
 CF981901
 EST.
 GI:38514950

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 50)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

McCarrey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Pape, D.,
 Martin, J., Wylie, T., Dante, M., Bowers, Y., Theising, B., Gibbons, M.,
 Ritter, E., Tsagaris, R., Ronko, I., Maguire, L., Kennedy, S.,
 Bennett, J., Waterston, R. and Wilson, R.
 NIEHS Mouse
 Unpublished (2002)
 Contact: McCarrey/Eddy NIEHS Mouse
 NIEHS Mouse
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

Library constructed and donated by J. McCarrey, Ph.D. (Southwest
 Foundation for Biomedical Research, Dept. of Genetics) - excision
 done by E.M. Eddy, Ph.D. (National Institutes of Health, National
 Institute of Environmental Health Sciences).
 Seq primer: Primer name ambiguous.

FEATURES
 source

1..50
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:7031702"
 /sex="male"
 /tissue_type="18-day preleptotene spermatocytes"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="McCarrey Eddy 18 day preleptotene
 spermatocytes"
 /note="Organ: testis; Vector: pBluescript SK+
 (Stratagene); Site 1: XhoII; Site 2: EcoRI; cDNA oligo
 dt-primed [5'-(GA)10-ACTAGTCGAGTTTCTTTT-3'] and
 directionally cloned using 5' linkers 5'-AATCGGCAGAG-3'
 and 5'-CTCGTGGC-3'. Size selection of >400bp material
 gives excised (from lambda-UniZAP-XR) and resulting
 mass excised (from lambda-UniZAP-XR) and resulting
 single-stranded phagemids were prepped and transformed into
 DH10B. Library constructed and donated by J. McCarrey,
 Ph.D. (Southwest Foundation for Biomedical Research, Dept.
 of Genetics); excision done by E.M. Eddy, Ph.D. (National
 Institutes of Health, National Institute of Environmental
 Health Sciences)."

ORIGIN

Query Match 14.1%; Score 23.2; DB 7; Length 50;
 Best Local Similarity 70.5%; Pred. No. 2.1e+04;
 Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 80 GACTGTCTTACCCCGGGAGGAGTCAGTCAGCCAGTCACAGCCC 123

Db 44 GCTAGTCTTACCCCGGGAGGATGTCAGTCAGCCAGCCAGCCC 1

RESULT 2
 CL639648/c

LOCUS
 DEFINITION
 P028B09 GGTG Gene Trap Library GV08C05 Mus musculus CDNA clone
 P028B09, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

CL639648 58 bp mRNA linear GSS 22-MAR-2005
 P028B09 GGTG Gene Trap Library GV08C05 Mus musculus CDNA clone
 P028B09, mRNA sequence.
 CL639648
 GSS.
 CL639648.3 GI:61686198
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 58)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBMED
 COMMENT

Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,
 Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.
 A large-scale, gene-driven mutagenesis approach for the functional
 analysis of the mouse genome
 Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
 12904583

On Mar 22, 2005 this sequence version replaced gi:58225660.
 Contact: GGTG
 German Genetrap Consortium (GGTC)
 Email: info@genetrap.de

FlipROSBetageo gene trap. Sequence tag generated by 5'RACE.
 Additional sequence information can be found at:
 'http://genetrap.gsf.de/project/web_new/database/result_clone.html?clone_id=P028B09'. ES cell line harboring insertion mutation of
 target gene is available at:
 'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm'
 1' Inhouse Sequence Identifier: 19838

Class: Gene Trap.

FEATURES
 source

Location/Qualifiers
 1..58
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129 Sv"
 /db_xref="taxon:10090"
 /clone="P028B09"
 /sex="Male"
 /cell_type="Embryonic stem cell"
 /cell_line="ES cells [C57BL/6J x 129Sv/SvEvTac] F1"
 /clone_lib="GGTC Gene Trap Library GV08C05"
 /note="Vector: FlipROSBetageo"

ORIGIN

Query Match 14.1%; Score 23.2; DB 10; Length 58;
 Best Local Similarity 65.4%; Pred. No. 2.2e+04;
 Matches 34; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 71 TCTGTGTTTACCTCTTACCCCGGGAGGAGTCAGTCAGCCAGTCACAGCCC 122

Db 53 TCTGCGAGAACATGCTTAATTCGCGGAGCGGGGAGGAGTCAGTCAGCCC 2

RESULT 3
 AZ791987/c

LOCUS
 DEFINITION
 2M0043G08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 clone UUGC2M0043G08 F, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AZ791987 71 bp DNA linear GSS 16-FEB-2001
 2M0043G08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 clone UUGC2M0043G08 F, genomic survey sequence.
 AZ791987
 GSS.
 AZ791987.1 GI:12935450
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 71)

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0043 row: G column: 08
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 71.

FEATURES source

1. .71
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0043G08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male); was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (9.1/4732114|gb|AF129072.1), a copy-number
inducible derivative of pAri29072.1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match
Best Local Similarity 13.2%; Score 21.6; DB 9; Length 71;
Matches 36; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 51 TTCTCAAGCAGGTCCTCTCTGTTGACTGTCTTACCCGGGAGGAGGAGCAGC 110
|||||
Db 61 TTCACACTGACAGTCTCTGTCCCTTTGAAGCCAGCGCCCTCTGTGTGAAGAACGC 2
|||||

RESULT 4
CV305418
LOCUS
ti62a05.b7 Mouse 5' RACE clones Mus musculus cDNA 5', mRNA
DEFINITION
Sequence.
ACCESSION
CV305418
VERSION
CV305418.1 GI:52622751
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE AUTHORS

1 (bases 1 to 72)
Dike, S., Balija, V.S., Nascimento, L.U., Xuan, Z., Ou, J., Zutavern, T.,
Palmer, L.E., Hannon, G., Zhang, M.Q. and McCombie, W.R.
TITLE
The mouse genome: Experimental examination of gene predictions and
transcriptional start sites
JOURNAL
Genome Res. 14 (12), 2424-2429 (2004)
PUBMED
15574821
COMMENT
Contact: Balija VS
McCombie Laboratory
Cold Spring Harbor Laboratory
500 Sunnyside Blvd, Woodbury, NY 11797, USA
Fax: 516 422 4109
Email: balija@cshl.org.

FEATURES source

1. .72
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone_lib="Mouse 5' RACE clones"
/note="Vector: PCR-TOPO2.1; Cloned 5' RACE fragments
amplified from 5' RACE cDNA generated from 15 pooled mouse
tissues and stages: 7, 11, 15, & 17-day total embryo,
whole brain, eye, kidney, liver, lung, prostate, and
submaxillary gland, smooth muscle, spleen, testes and
uterus."

ORIGIN

Query Match
Best Local Similarity 12.9%; Score 21.2; DB 7; Length 72;
Matches 35; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 40 CAGTCCCGAAGTTCTCAAGGCACAGGTCTCTTCCTGGTTGACTGTCTTACCCGGG 97
|||||
Db 8 CAGTGAAGCATCTCTTCAGAGTCTCAACTCATCTCTTGGAAAGTCTCTGACGACGAG 65
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RESULT 5 CV305419/c

LOCUS
ti62a05.g7 Mouse 5' RACE clones Mus musculus cDNA 5', mRNA
DEFINITION
Sequence.
ACCESSION
CV305419
VERSION
CV305419.1 GI:52622752
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE AUTHORS

1 (bases 1 to 72)
Dike, S., Balija, V.S., Nascimento, L.U., Xuan, Z., Ou, J., Zutavern, T.,
Palmer, L.E., Hannon, G., Zhang, M.Q. and McCombie, W.R.
TITLE
The mouse genome: Experimental examination of gene predictions and
transcriptional start sites
JOURNAL
Genome Res. 14 (12), 2424-2429 (2004)
PUBMED
15574821
COMMENT
Contact: Balija VS
McCombie Laboratory
Cold Spring Harbor Laboratory
500 Sunnyside Blvd, Woodbury, NY 11797, USA
Fax: 516 422 4109
Email: balija@cshl.org.

FEATURES source

1. .72
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone_lib="Mouse 5' RACE clones"
/note="Vector: PCR-TOPO2.1; Cloned 5' RACE fragments
amplified from 5' RACE cDNA generated from 15 pooled mouse
tissues and stages: 7, 11, 15, & 17-day total embryo,
whole brain, eye, kidney, liver, lung, prostate,
submaxillary gland, smooth muscle, spleen, testes and

```

ORIGIN
Query Match      12.9%; Score 21.2; DB 7; Length 72;
Best Local Similarity 60.3%; Pred. No. 9.8e+04;
Matches 35; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 40 CAGTCCGAGTCTCTCAAGGCACAGGTCTCTCTCTGTTGACTGTCTTACCCCGG 97
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65 CAGTGAAGCATCTCTTCAGAGTCTGAAGTCTATCTCTGTTGAAAGTCTGACGACGAG 8

RESULT 6
LOCUS BJ083039/c
DEFINITION BJ083039 NIBB Mochii normalized xenopus tailbud library Xenopus
            laevis cDNA clone XL083017 3', mRNA sequence.
ACCESSION BJ083039
VERSION BJ083039.1 GI:17577941
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
          Xenopodinae; Xenopus; Xenopus.
          1 (bases 1 to 66)
REFERENCE Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
AUTHORS Kohara,Y.
TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadasu Shin-i
          Center For Genetic Resource Information
          National Institute of Genetics
          1111 Yata, Mishima, Shizuoka 411-8540, Japan
          Tel: 81-559-81-6856
          Fax: 81-559-81-6855
          Email: tshini@genes.nig.ac.jp
          The information of this clone is available through the following
          URL.
          http://xenopus.nibb.ac.jp.
FEATURES
    source
    Location/Qualifiers
        1..66
        /organism="Xenopus laevis"
        /mol_type="mRNA"
        /db_xref="taxon:8355"
        /clone="XL083017"
        /tissue_type="whole embryo"
        /dev_stage="stage 25"
        /clone.lib="NIBB Mochii normalized Xenopus tailbud
        library"

ORIGIN
Query Match      12.7%; Score 20.8; DB 3; Length 66;
Best Local Similarity 60.7%; Pred. No. 1.3e+05;
Matches 34; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 107 CAGCAGCTGACGCCCCAGTGAAGACATCTGACCTCAATCCAGATAGTGA 162
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 CATCAACCTATTCTAGCCAAATGTGATGATACATCTGCTTTACCTCGACATATGTA 6

RESULT 7
LOCUS H84929/c
DEFINITION H84929 yv85h01.s1 Soares melanocyte 2N5HM Homo sapiens cDNA clone
            IMAGE:249553 3', similar to gb:222548 THIOI-SPECIFIC ANTIOXIDANT
            PROTEIN (HUMAN);, mRNA sequence.
ACCESSION H84929
VERSION H84929.1 GI:1064424
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominoidea; Homo.
          1 (bases 1 to 75)
REFERENCE Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
AUTHORS Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
          Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,P.,
          Trevisakis,E., Waterston,R., Williamson,A., Wohldmann,P. and
          Wilson,R.
          The WashU-Merck EST Project
          Unpublished (1995)
          Contact: Wilson RK
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: est@watson.wustl.edu
          High quality sequence starts: 1
          High quality sequence stops: 1
          Source: IMAGE Consortium, LLNL
          This clone is available royalty-free through LLNL; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          Trace considered overall poor quality
          Seq primer: Promega -21ml3
          High quality sequence stop: 1.
          Location/Qualifiers
              1..75
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="GDB:3867259"
              /db_xref="taxon:9606"
              /clone="IMAGE:249553"
              /sex="Male"
              /tissue_type="melanocyte"
              /lab_host="DH10B (ampicillin resistant)"
              /clone.lib="Soares melanocyte 2N5HM"
              /note="Vector: pT7T3D (Pharmacia) with a modified
              polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
              was primed with a Not I - oligo(dT) primer [5'
              TGTTCACCAATCTGAAGTGGAGCGCGCCGAGTTTTTTTTTTTTTTT 3'],
              double-stranded cDNA was size selected, ligated to Eco RI
              adapters (Pharmacia), digested with Not I and cloned into
              the Not I and Eco RI sites of a modified pT7T3 vector
              (Pharmacia). Library constructed by Bento Soares and
              M.Fatima Ronaldo. RNA from normal foreskin melanocytes
              (FS374) was kindly provided by Dr. Anthony P. Albino."

ORIGIN
Query Match      12.7%; Score 20.8; DB 8; Length 75;
Best Local Similarity 58.6%; Pred. No. 1.3e+05;
Matches 34; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 72 CCTGTTTGCATGTCCTTACCCGGGAGGCGAGTGCAGCCAGCTGCAAGCCCAAGT 129
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 72 CCTNGGTNCCCTATGCTGACCCAGGAAGGCCAGGCGCTGCCCTCCAGACTCGCAGT 15

RESULT 8
LOCUS AZ768319/c
DEFINITION AZ768319 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0568E17 F, genomic survey sequence.
ACCESSION AZ768319
VERSION AZ768319.1 GI:12887304
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Murioidea; Muridae; Murinae; Mus.
          1 (bases 1 to 67)
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
AUTHORS Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

```

TITLE
Niederhauser, A. and Wright, D., Weiss, R.
JOURNAL
Mouse whole genome scaffolding with paired end reads from 10kb
COMMENT
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0568 row: E column: 17
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 67.

FEATURES

Location/Qualifiers
1..67
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0568E17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells, and selected for ampicillin resistance."

ORIGIN

Query Match 12.6%; Score 20.6; DB 9; Length 67;
Best Local Similarity 62.7%; Pred. No. 1.5e+05;
Matches 32; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 21 GGGACTGGCAGTTCAGACGTCGCGAGTTCCTCAAGGACAGGTCCTCTT 71
|||||
DB 52 GGGACAGCCCATCTCTAGTCGAGATGCAATACCTCAATATCATGTATCTT 2
|||||

RESULT 9
CL603643/c
LOCUS
DEFINITION
CH240_178P06.TV CHORI-240 Bos taurus genomic clone CH240_178P06,
genomic survey sequence.

ACCESSION
CL603643
VERSION
CL603643.1 GI:48871675
KEYWORDS
GSS.

SOURCE
Bos taurus (cow)
ORGANISM
Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Fecora; Bovidae; Bovinae; Bos.

REFERENCE
Costa, J.N., Mota, M. and Caetano, A.R.
1 (bases 1 to 74)

AUTHORS
Brazil's Contribution to End-Sequencing the Bovine BAC Library

TITLE

JOURNAL COMMENT

Unpublished (2003)
Other GSSs: CH240_178P06.TV
Contact: Caetano AR
Department of Biotechnology
Embrapa Recursos Geneticos e Biotecnologia
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.
02372, 70770-900 Brasil
Tel: 55 61 448 4778
Fax: 55 61 340 3658
Email: acaetano@embrapa.br
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm).
Bases shown have Phred quality value equal to or higher than 20.
Bases with quality value below 20 were masked with 'N'.
For BAC library availability, please contact Pieter de Jong
(pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm).
This work was undertaken as part of the International Bovine BAC
Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e
Biotecnologia with financing from Conselho Nacional de
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil
Plate: 178 row: P column: 06
Seq primer: 77
Class: BAC ends
High quality sequence stop: 74.

FEATURES

Location/Qualifiers
1..74
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_178P06"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 12.6%; Score 20.6; DB 10; Length 74;
Best Local Similarity 47.8%; Pred. No. 1.5e+05;
Matches 32; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 89 TACCCGGGAGGAGTGCAGCCAGCTGCAAGCCCCCAGTCAAGACATCTGAGCTCA 148
|||||
DB 74 TAACCGTGAAGAAGAGAGCGAAAGCAANNNNNNNNNGAAGATATAAGNNNNNA 15
|||||

QY 149 ATCCAGA 155
|||||
DB 14 ATGCAGA 8
|||||

RESULT 10

LOCUS
DQ051485/c

DEFINITION
Pan troglodytes SOD3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION
DQ051485

VERSION
DQ051485.1 GI:66904687

KEYWORDS
GSS.

SOURCE
Pan troglodytes (chimpanzee)

ORGANISM
Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.

REFERENCE
1 (bases 1 to 80)

AUTHORS
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fedel-Alon, A., Tanenbaum, D.M., Civallo, D.,
White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

TITLE
A Scan for Positively Selected Genes in the Genomes of Humans and

```

Chimpanzees
(er) PLOS Biol. 3 (6), E170 (2005)
15869325
REFERENCE
AUTHORS
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE
Direct Submission
JOURNAL
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES
source
1..80
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>80
/gene="SOD3"
/locus_tag="HC19509"
ORIGIN
Query Match 12.6%; Score 20.6; DB 11; Length 80;
Best Local Similarity 67.4%; Pred. No. 1.6e+05;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 122 CCCACAGTGAAGAACATCTGAGCTCAATTCAGATAGTGACA 164
|||||
Db 72 CCCACCGTGAAGATCCCAATGAGATCATCATCTGCCCGCATGTGACA 30
|||||

RESULT 11
AZ829920/c
LOCUS
DEFINITION
2M0107A19R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0107A19 R, genomic survey sequence.
ACCESSION
AZ829920
VERSION
GSS.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 60)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0107 Row: A Column: 19
Seq primer: CACACGAGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 60.
FEATURES
source
1..60
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0107A19"

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI4732114|9b|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 12.4%; Score 20.4; DB 9; Length 60;
Best Local Similarity 61.1%; Pred. No. 1.7e+05;
Matches 33; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Qy 108 AGCCAGCTGCAAGCCCCCAGTGAGAACATCTGAGCTCAATTCAGATAAGTG 161
|||||
Db 57 AGTAAAGTGTAGCTTTCAGGCACCGACCATCTGAGTCAAGCCCAAGAAAGAG 4
|||||

RESULT 12
AA917946
LOCUS
DEFINITION
ol68g04.s1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1534806 3',
similar to TR:Q07611 Q07611 PROLINE-RICH PROTEOLYCAN PRP2.
;contains MSRI.t3 MSRI repetitive element ;, mRNA sequence.
ACCESSION
AA917946
VERSION
AA917946.1 GI:3057836
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 79)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES
source
1..79
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1534806"
/lab_host="DH10B"

```

/clone lib="NCI CGAP_Kid3"
 /note="Organ: kidney; Vector: pTT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 12.4%; Score 20.4; DB 1; Length 79;
 Best Local Similarity 65.2%; Pred. No. 1.8e+05;
 Matches 30; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 27 GGCAGTTCCTAGACAGTCCGAGTCTCTCAAGGCACAGGTCTCTTC 72
 |||||
 Db 9 GGACCTTGCTCCACATCCCACTCCCTCGGAGGCGCCCTTC 54
 |||||

RESULT 13

CG869849/c
 LOCUS
 DEFINITION XS0340 Sanger Institute Gene Trap Library pGT01xf Mus musculus

CG869849
 cDNA, mRNA sequence.

ACCESSION CG869849

VERSION CG869849.2 GI:60335575

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 57)

AUTHORS Sanger Institute Gene Trap Resource - SIGTR.

TITLE http://www.sanger.ac.uk/PostGenomics/genetrap/

JOURNAL Unpublished (2003)

COMMENT On Feb 25, 2005 this sequence version replaced gi:38533529.

Contact: Sanger Institute Gene Trap Resource - SIGTR

Wellcome Trust Sanger Institute

Email: info.genetrap@sanger.ac.uk

Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from Sanger Institute Gene Trap Resource. Annotation information available from http://www.sanger.ac.uk/PostGenomics/genetrap/

Class: Gene Trap.

Location/Qualifiers

1..57

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129 OLA"

/db_xref="taxon:10090"

/sex="Male"

/cell_type="Embryonic Stem Cell"

/clone_lib="Sanger Institute Gene Trap Library pGT01xf"

/note="Vector: pGT01xf"

ORIGIN

Query Match 12.3%; Score 20.2; DB 10; Length 57;
 Best Local Similarity 59.6%; Pred. No. 1.9e+05;
 Matches 34; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 39 ACAGTCCGAGTCTCAGGCACAGTCTCTCTCGTTTACTCTCTTACCTTACCCCG 95
 |||||

Db 57 AAAACCCGATCTGCTGAGGCACAGCCCGGAGGTGGAGGCTCTCTCCCG 1
 |||||

RESULT 14

CL640815/c
 LOCUS
 DEFINITION M079B07 GGTc Gene Trap Library GV07C04 Mus musculus cDNA clone

M079B07, mRNA sequence.

ACCESSION

VERSION CL640815

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

On Mar 22, 2005 this sequence version replaced gi:49489262.

Contact: GGTc

German Genetrap Consortium (GGTC)

Email: info@genetrap.de

U3CEO gene trap. Sequence tag generated by 5' RACE. Additional

sequence information can be found at:

'http://genetrap.gsf.de/project/web_new/database/result_clone.html'

clone_id=M079B07, ES cell line harboring insertion mutation of

target gene is available at:

'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm'

1' Inhouse Sequence Identifier: 14819

Class: Gene Trap.

Location/Qualifiers

1..74

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129 Sv"

/db_xref="taxon:10090"

/clone="M079B07"

/sex="Male"

/cell_type="Embryonic stem cell"

/cell_line="ES cells 129S2 (formerly 129/SvPas)"

/clone_lib="GGTC Gene Trap Library GV07C04"

/note="Vector: U3CEO"

ORIGIN

Query Match 12.3%; Score 20.2; DB 10; Length 74;

Best Local Similarity 63.3%; Pred. No. 2.1e+05;

Matches 31; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 116 GCAAGCCCACTGAGGACATCTGAGCTCAATCCAGATGACGACA 164
 |||||

Db 60 GTAAGACACTTGTAAGAGAACTGAAGACATTTACAGATAACAGAGA 12
 |||||

RESULT 15

AKI98748

LOCUS

DEFINITION

Mus musculus cDNA, clone: Y1G0129B02, strand: minus,

reference: ENSMUSBL:Mouse-Transcript-ENST:ENSMUST00000002683, based

on BLAT search.

ACCESSION AKI98748

VERSION AKI98748.1 GI:56022925

KEYWORDS HTC; ASSETS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

2 (bases 1 to 77)

Watahiki, A., Waki, K., Hayatsu, N., Shiraki, T., Kondo, S.,

Nakamura, M., Sasaki, D., Arakawa, T., Kawai, J., Harbers, M.,

Hayashizaki, Y., and Carninci, P.

Libraries enriched for alternatively spliced exons reveal splicing

patterns in melanocytes and melanomas

Nat. Methods 1, 233-239 (2004)

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

2 (bases 1 to 77)

Watahiki, A., Waki, K., Hayatsu, N., Shiraki, T., Kondo, S.,

Nakamura, M., Sasaki, D., Arakawa, T., Kawai, J., Harbers, M.,

Hayashizaki, Y., and Carninci, P.

Libraries enriched for alternatively spliced exons reveal splicing

patterns in melanocytes and melanomas

Nat. Methods 1, 233-239 (2004)

REFERENCE

2 (bases 1 to 77)

AUTHORS
Arakawa, T., Carninci, P., Fukuda, S., Harbers, M., Hayatsu, N.,
Hori, F., Imotani, K., Kawai, J., Kondo, S., Murata, M., Nakamura, M.,
Nomura, K., Ono, M., Sasaki, D., Shiraki, T., Waki, K., Watahiki, A., and
Havashizaki, Y.

TITLE
JOURNAL

Direct Submission
Submitted (15-SEP-2004) Yoshihide Hayaishizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama,
Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URI: http://genome.gsc.riken.jp, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT

Alternative Splicing Libraries (ASLs) are prepared by: Preparing of single-stranded DNA using a RNA template from full length cDNA libraries, hybridizing of single-stranded DNAs, removing of remaining single-stranded DNA, digesting of regions comprising double-stranded DNA by a set of 4 bp-cutters, capturing of DNA hybrids with loop structures (alternative spliced exon), ligating of Y-shaped primers to isolated DNA hybrids with loop structures, PCR amplification of ligation products and their cloning into pTET1 vector (reference).

FEATURES	source
Location/Qualifiers	1..77
	/organism="Mus musculus"
	/mol_type="mRNA"
	/db_xref="taxon:10090"
	/clone="Y1G0129802"
	/cell_line="mixture of B16-F10Y and melan-c"
	/cell_type="mixture of melanoma cell and melanocyte cell"
	/clone_lib="Alternative Splicing Library L1"
	/note="strand:minus, reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST0000002683, based on BLAT search"

ORIGIN		Query Match				Score 20.2; DB 4; Length 77;			
		Best Local Similarity 63.3%; Pred. No. 2.1e+05;							
		Matches 31; Conservative 0; Mismatches 18; Indels 0; Gaps 0;							
QY	3	TCGGCCACCTTTGTATGAGGGGACTTGGGCAGTTC	TCAGACAGTCCCGAAGT	51					
Db	23	TCGGCCATCTCCGTGGAGACACCGTCTGATTTCTACTGTGCCAGGT	71						

RESULT 16	BG237470	LOCUS	BG237470	72 bp	mRNA	linear	EST 23-JUL-2004
DEFINITION	sab07a06.y1 Gm-cl071 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl071-780 5', mRNA sequence.						

ACCESSION	BG237470	GI:12772616
VERSION	BG237470.1	
KEYWORDS	EST.	
SOURCE	Glycine max (soybean)	
ORGANISM	Glycine max	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; eudicotyledons; core eudicotyledons; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.	

1. (bases 1 to 72)

REFERENCES

AUTHORS

Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucabara, F., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibson, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.

TITLE	COMMENT
Public Soybean EST Project	Public Soybean EST Project
Unpublished (1999)	Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project	Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project	Public Soybean EST Project
Washington University School of Medicine	Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800	Tel: 314 286 1800
Fax: 314 286 1810	Fax: 314 286 1810
Email: est@watson.wustl.edu	Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. Putative full length read vector to vector length is 81 This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com).

```

FEATURES
source
Location/Qualifiers
1..72
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl071-780"
/tissue_type="immature pods (~2cm long) of greenhouse
grown plants"
/lab_host="DH10B"
/clone_lib="Gm-cl071"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; The
cDNA library was constructed from mRNA isolated from
immature pods (approximately 2cm long) of greenhouse grown
plants. The library was prepared using the Life
Technologies pSuperScript cDNA library construction kit.
Complementary DNA was synthesized from mRNA using a
poly(dT) sequence with a NotI restrictions site. SalI
linkers adapters were ligated to the blunt-ended cDNA
fragments followed by NotI digestion. The cDNA fragments
were directionally cloned into the NotI-SalI restriction
site of the pSPORT1 vector. The ligated cDNA fragments
were transformed into E.coli ElectroMax DH10B host cells.
This library was constructed in the laboratory of Dr. Lila
Vodkin by Anu Khanna at the University of Illinois at
Urbana-Champaign. email: l-vodkin@uiuc.edu."

```

[illegible]

RESULT 17	AF149527	LOCUS	AF149527	64 bp	DNA	linear	GSS 12-JUN-2000
DEFINITION	AF149527		Human chromosome 18q21 from exon-trapping Homo sapiens genomic clone 1b18. genomic survey sequence.				

ACCESSION	AF149527	Accession #	Sequence Survey
VERSION	AF149527.1	GI:	8485853
KEYWORDS	GSS.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa;		
	Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		

REFERENCE
1 (bases 1 to 64)
AUTHORS
Chen, H., Huo, Y., Patel, S., Zhu, X., Swift-Scanlan, T., Reeves, R. H., DePaulo, R. Jr., Ross, C. A. and McInnis, M. G.
TITLE
Gene identification using exon amplification on human chromosome 18q21: implications for bipolar disorder
JOURNAL
Mol. Psychiatry 5 (5), 502-509 (2000)

11032383	<p> Contact: Chen H Psychiatry and Behavioral Sciences Johns Hopkins University School of Medicine 600 N. Wolfe Street, Baltimore, MD 21287, USA Email: hc@welchlink.welch.jhu.edu Class: exon-trapped. </p>
----------	---

```

FEATURES
source
Location/Qualifiers
1..64
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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/clip="18q21"
/clone="1p18"
/clone_lib="Human chromosome 18q21 from exon-trapping"

ORIGIN
Query Match      12.1%; Score 19.8; DB 9; Length 64;
Best Local Similarity 69.2%; Pred. No. 2.7e+05;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 95 GGGAGGAGTCGACGAGTCGACGAGCCCAAGCCCAAGTCGAG 133
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 22 GAGGATGCCAAGCAGCCTGTGGGAAGCCACGCGTGAAG 60

RESULT 18
AZ615721/c
LOCUS      AZ615721
DEFINITION 1M0445N01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0445N01 F, genomic survey sequence.
ACCESSION  AZ615721
VERSION     AZ615721.1 GI:11737827
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

REFERENCE
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
          University of Utah Genome Center
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: dunn@genetics.utah.edu
          Insert length: 10000 Std. Error: 0.00
          Plate: 0445 row: N column: 01
          Seq primer: CGTTGTAAACGACGCGCAGT
          Class: plasmid ends
          High quality sequence stop: 77.
          Location/Qualifiers
            1. .77
              /organism="Mus musculus"
              /mol_type="genomic DNA"
              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /clone="UUGC1M0445N01"
              /sex="Male"
              /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
              /clone_lib="Mouse 10kb plasmid UUGC1M library"
              /notes="Vector: pWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adapted DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 [gi|4732114|gb|AF129072.1|], a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and

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purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match      12.1%; Score 19.8; DB 9; Length 77;
Best Local Similarity 63.8%; Pred. No. 2.8e+05;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 96 GGGAGGAGTCGACGAGTCGACGAGCCCAAGCCCAAGTCGAGACATCTGA 142
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 63 GGCAGACAGTCCAGAAAGATGCCCAAGCCCAAGTCGACTACATCAGA 17

RESULT 19
AG829487
LOCUS      AG829487
DEFINITION Sus scrofa DNA, BAC clone L243P12, shotgun sequence of subclone
L243P12S002E03, read with -21M13 primer, genomic survey sequence.
ACCESSION  AG829487
VERSION     AG829487.1 GI:56375985
KEYWORDS   GSS.
SOURCE     Sus scrofa (pig)
ORGANISM   Sus scrofa

REFERENCE
AUTHORS   Tanaka,M., Suzuki,K., Morozumi,T., Kobayashi,E., Matsumoto,T.,
          Domukai,M., Eguchi-Ogawa,T., Shinkai,H., Awata,T. and Uenishi,H.
          Genomic structure of the distal extended-class II region in swine
          Unpublished
          2 (bases 1 to 80)
          Uenishi,H., Tanaka,M. and Awata,T.
          Direct Submission
          Submitted (25-OCT-2004) Hirohide Uenishi, National Institute of
          Agrobiological Sciences, Animal Genome Laboratory, Genome Research
          Department; 2 Ikenodai, Tsukuba, Ibaraki, 305-8602, Japan
          (E-mail:huenishi@affrc.go.jp, Tel:81-29-838-8627,
          Fax:81-29-838-8627)
          Correspondence to:
          Hirohide Uenishi
          Animal Genome Laboratory, Genome Research Department, National
          Institute of Agrobiological Sciences
          2 Ikenodai, Tsukuba, Ibaraki 305-8602, JAPAN
          Tel: +81-29-838-8627
          Fax: +81-29-838-8627
          e-mail: huenishi@affrc.go.jp
          Sequencing was carried out in Animal Genome Research Program
          (Japan)
          by National Institute of Agrobiological Sciences
          and STAFF-Institute.
          Subclones of BAC clones were constructed with pUC18 vector.
          Basecalling was performed by Phred 0.020425.c.
          Vector sequences were eliminated by crossmatch version 0.990319.
          Low quality bases were trimmed based on the quality values with the
          aid of the trim-alt option of Phred.
          Location/Qualifiers
            1. .80
              /organism="Sus scrofa"
              /mol_type="genomic DNA"
              /db_xref="taxon:9823"
              /clone="L243P12"
              /sub_clone="L243P12S002E03"
              /clone_lib="Sus scrofa shotgun BAC sequence"

ORIGIN
Query Match      12.1%; Score 19.8; DB 10; Length 80;
Best Local Similarity 77.4%; Pred. No. 2.8e+05;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 79 TGACTGTCTTACCCCGGAGGAGTCGAG 109

```



```

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

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ORIGIN

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Query Match 12.0%; Score 19.6; DB 10; Length 74;
Best Local Similarity 66.7%; Pred. No. 3.2e+05;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 100 GGCAGTGCACGACGAGTGCAGCCGACAGTGAAGAACATCTG 141
      |||||
DB 49 GGCAGTGCACGAGCGATCCGATCTCCACAGAGACAGACCTG 8

```

```

RESULT 23
LOCUS AG217126 78 bp DNA linear GSS 03-SRP-2002
DEFINITION Drosophila melanogaster DNA, clone:NP7083-5-1, flanking P[GawB] transposon insertion, genomic survey sequence.
ACCESSION AG217126
VERSION AG217126.1 GI:22764126
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster

```

```

REFERENCE 1
AUTHORS Hayaishi, S., Ito, K., Sado, Y., Taniguchi, M., Akimoto, A., Takeuchi, H., Aigaki, T., Matsuzaki, F., Nakagoshi, H., Tanimura, T., Ueda, R., Uemura, T., Yoshihara, M. and Goto, S.
TITLE GETDB, a database compiling expression patterns and molecular locations of a collection of Gal4 enhancer traps
JOURNAL Genesis (2002) In press
REFERENCE 2 (bases 1 to 78)
AUTHORS Hayaishi, S.

```

```

TITLE Direct Submission
JOURNAL Submitted (27-AUG-2002) Shigeo Hayaishi, RIKEN Center for Developmental Biology, Laboratory for Morphogenetic Signaling; Chuo-ku, Minatojima-ninamachi 2-2-3, Kobe, Hyogo 650-0047, Japan (E-mail: shayaishi@cdb.riken.go.jp, Tel: 81-78-301-3184, Fax: 81-78-301-3183)
COMMENT This clone was isolated from genomic DNA flanking an insertion of the P element vector P[GawB] of a Drosophila strain.
FEATURES
source
1..78
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="NP7083"
/db_xref="taxon:7227"
/chromosome="2"
/map="42B3"
/notes="flanking P[GawB] transposon insertion"

```

ORIGIN

```

Query Match 12.0%; Score 19.6; DB 10; Length 78;
Best Local Similarity 54.1%; Pred. No. 3.2e+05;
Matches 40; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 78 TTGACTGTCTTACCCGGGAGGAGTGCAGCCAGTGCAGCCAGCCAGTGAAGAACAA 137
      |||||
DB 5 TGGTCTGCACACCGACAGACAGAGCGGCCGAGTCCGAGCGCCGAAGGGCGCTCA 64

QY 138 TCTGAGCTCAATC 151
      |||||
DB 65 TTTTAGAGCAGATC 78

RESULT 24
LOCUS TAl12C05Q 59 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 112C05, reverse sequence, genomic survey sequence.
ACCESSION AL462137
VERSION AL462137.1 GI:11832263
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 59)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhleasanger@cbi.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
source
1..59
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="112C05"
ORIGIN
Query Match 11.8%; Score 19.4; DB 11; Length 59;
Best Local Similarity 70.3%; Pred. No. 3.5e+05;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 74 TGGTTTGACTGTCCTTACCCGGGAGGAGTGCAGTGCAGC 110
      |||||
DB 2 TCGTGTGAATGTCTTTTACCTCGTCGACACTGTAGC 38

RESULT 25
LOCUS CG638372 62 bp mRNA linear GSS 02-OCT-2003
DEFINITION OST367812 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST367812, mRNA sequence.
ACCESSION CG638372
VERSION CG638372.1 GI:37462221
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

```

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 62)

REFERENCE
 AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
 Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
 Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
 Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
 Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
 Sparks, M.J., van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
 Zhu, Q., Person, C. and Sands, A.T.
 Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 14610273

TITLE
 JOURNAL
 PUBMED
 COMMENT
 Contact: Zambrowicz BP
 OmniBank
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.
 Location/Qualifiers
 1..62
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST367812"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129Sv/Ev"

FEATURES
 source
 1..62
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST367812"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129Sv/Ev"

ORIGIN
 Query Match 11.8%; Score 19.4; DB 10; Length 62;
 Best Local Similarity 64.4%; Pred. No. 3.5e+05;
 Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
 Qy 65 GTCTCTTCCTGGTTGACTGCTTACCCGGGAGGAGTGCGAG 109
 |||||
 Db 16 GTGTGTACTGGTTTGCTTCACGTCGCCCATGGAAGCCAGAAGAG 60
 |||||

Search completed: March 3, 2006, 11:01:18
 Job time : 8979.05 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:16:16 ; Search time 376.932 Seconds
(without alignments)
2714.499 Million cell updates/sec

Title: US-10-655-801-19
Perfect score: 18
Sequence: 1 catcaagggtgcgcgaga 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5983141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2389942

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_in.*
- 3: gb_env.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sts.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vi.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.8	76.7	47	6	E07475
C 2	13.8	76.7	74	15	ATH525630
C 3	13.4	74.4	39	6	Q0801018
C 4	13.4	74.4	44	6	AX206894
C 5	13.4	74.4	45	6	AX146612
C 6	13.4	74.4	65	6	Q0532654
C 7	13.2	73.3	23	2	CEL487557
C 8	13.2	73.3	23	2	DME421757
C 9	13.2	73.3	23	2	DME421758
C 10	13.2	73.3	23	6	Q0873596
C 11	13.2	73.3	51	6	Q0069930
C 12	13.2	73.3	68	6	AX233504
C 13	13.2	73.3	76	6	Q0874036
C 14	13.2	73.3	80	9	S76293
C 15	13	72.2	18	6	AR086069
C 16	13	72.2	18	6	AR140423
C 17	13	72.2	18	6	AR146904
C 18	13	72.2	33	8	HSA403872
C 19	12.8	71.1	19	6	AX727459
C 20	12.8	71.1	20	6	AR164017
C 21	12.8	71.1	20	6	AX059371
C 22	12.8	71.1	23	6	Q0890713
C 23	12.8	71.1	23	6	Q0897253
C 24	12.8	71.1	23	6	Q0898402
C 25	12.8	71.1	27	6	AX206899
C 26	12.8	71.1	35	6	AX931869
C 27	12.8	71.1	37	6	E11529
C 28	12.8	71.1	38	6	E07474
C 29	12.8	71.1	52	6	A22368
C 30	12.8	71.1	52	6	AR076116
C 31	12.8	71.1	57	9	MUSIGHMQ2
C 32	12.8	71.1	60	6	Q0553838
C 33	12.8	71.1	65	6	Q0531035
C 34	12.8	71.1	65	6	Q0534516
C 35	12.8	71.1	65	6	Q0554931
C 36	12.8	71.1	65	6	Q0556308
C 37	12.8	71.1	75	6	CS110174
C 38	12.4	68.9	19	6	AR571546
C 39	12.4	68.9	19	6	AX129656
C 40	12.4	68.9	20	6	BD133801
C 41	12.4	68.9	20	6	AX469759
C 42	12.4	68.9	24	6	AR217119
C 43	12.4	68.9	24	6	AX099239
C 44	12.4	68.9	27	6	AR028551
C 45	12.4	68.9	32	6	AX206898
C 46	12.4	68.9	33	6	AX828628
C 47	12.4	68.9	39	15	ATH551668
C 48	12.4	68.9	40	11	CS000192
C 49	12.4	68.9	45	6	AR217113
C 50	12.4	68.9	51	6	Q001515
C 51	12.4	68.9	51	6	Q0005999
C 52	12.4	68.9	60	6	Q0537961
C 53	12.4	68.9	77	6	Q0979038
C 54	12.2	67.8	20	6	AR160928
C 55	12.2	67.8	20	6	Q0878663
C 56	12.2	67.8	20	6	AX473981
C 57	12.2	67.8	20	6	AX448320
C 58	12.2	67.8	21	6	AX664291
C 59	12.2	67.8	21	6	Q0933286
C 60	12.2	67.8	22	6	AR612404
C 61	12.2	67.8	22	6	AX342375
C 62	12.2	67.8	24	6	BD142821
C 63	12.2	67.8	24	6	AX446606
C 64	12.2	67.8	30	6	A42595
C 65	12.2	67.8	30	6	A88783
C 66	12.2	67.8	30	6	AR149763
C 67	12.2	67.8	30	6	BD066296
C 68	12.2	67.8	30	6	BD130647
C 69	12.2	67.8	30	6	AR285590
C 70	12.2	67.8	30	6	AR404882
C 71	12.2	67.8	30	6	AR654614
C 72	12.2	67.8	34	6	BD225214
C 73	12.2	67.8	34	6	AX399454
C 74	12.2	67.8	34	6	Q002546
C 75	12.2	67.8	50	6	Q0808850
C 76	12.2	67.8	51	6	Q0007506
C 77	12.2	67.8	51	6	AX204242
C 78	12.2	67.8	53	6	I08081
C 79	12.2	67.8	59	6	BD194944
C 80	12.2	67.8	59	6	Q0855463
C 81	12.2	67.8	60	6	Q0537531
C 82	12.2	67.8	60	6	Q0539496
C 83	12.2	67.8	65	6	Q0555569
C 84	12.2	67.8	77	6	AX187656
C 85	12	66.7	28	6	Q0874790
C 86	12	66.7	30	6	AX328457
C 87	12	66.7	48	6	Q0848157
C 88	12	66.7	48	6	CS122771
C 89	12	66.7	50	6	Q0008400
C 90	12	66.7	50	6	AX160392
C 91	12	66.7	51	6	AX160391

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c 92 12 66.7 60 6 CQ538792 Sequence
c 93 12 66.7 65 6 CQ552279 Sequence
c 94 11.8 65.6 17 6 BD241406 Methods a
95 11.8 65.6 17 6 CQ622510 Sequence
96 11.8 65.6 17 6 CQ622511 Sequence
97 11.8 65.6 17 6 CQ622512 Sequence
98 11.8 65.6 17 6 AR466573 Sequence
99 11.8 65.6 17 6 AR466574 Sequence
100 11.8 65.6 17 6 AR466575 Sequence

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ALIGNMENTS

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RESULT 1
LOCUS E07475/c 47 bp DNA linear PAT 29-SEP-1997
DEFINITION Oligonucleotides for PCR probe.
ACCESSION E07475
VERSION E07475.1 GI:2175613
KEYWORDS JP 1994133780-A/6.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 47)
AUTHORS Negoro, T. and Tanaka, N.
TITLE NEW MODIFIED T-PA
JOURNAL Patent: JP 1994133780-A 6 17-MAY-1994;
SUMITOMO PHARMACEUT CO LTD
COMMENT OS None
OC Artificial sequences.
PN JP 1994133780-A/6
PD 17-MAY-1994
PF 23-OCT-1992 JP 1992309285
PI NEGORO TAKATSU, TANAKA NAOMI
PC C12N15/58,A61K37/54,C07K15/06,C07K15/14,C12N1/21, PC
C12N5/10//C12P21/02,
PC (C12N1/21,C12R1:19), (C12N5/10,C12R1:91), (C12P21/02,C12R1:19),
PC (C12P21/02,
PC (C12R1:91);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: Yes;
FH Key
FT Location/Qualifiers
FT source 1..47
FT misc_feature 1..47 /organism='Artificial sequences' FT
FT /note='Oligonucleotide IKGR'.
FEATURES
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1..47
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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ORIGIN
Query Match 76.7%; Score 13.8; DB 6; Length 47;
Best Local Similarity 88.2%; Pred. No. 6.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 CATCAAGGCGCCGAG 17
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Db 39 CATCAAGGCGCCTAG 23
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RESULT 2
LOCUS ATH525630 74 bp DNA linear PLN 29-MAR-2003
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 101G06.
ACCESSION AJ525630
VERSION AJ525630.1 GI:26793866

```

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KEYWORDS left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED 12446565
REFERENCE 2 (bases 1 to 74)
AUTHORS Balzerque, S.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

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FEATURES
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Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="101G06"
/ecotype="Wassilewskija"

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/note="T-DNA flanking sequence
left border"

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ORIGIN

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Query Match 76.7%; Score 13.8; DB 15; Length 74;
Best Local Similarity 83.3%; Pred. No. 7.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 CATCAAGGCGCCGAGA 18
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Db 24 CATCACACGTGGCCGNGA 41
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RESULT 3
LOCUS CQ801018/c 39 bp DNA linear PAT 05-MAY-2004
DEFINITION Sequence 9 from Patent WO2004033728.
ACCESSION CQ801018
VERSION CQ801018.1 GI:47057790
KEYWORDS synthetic construct
SOURCE other sequences; artificial sequences.
ORGANISM

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REFERENCE 1
AUTHORS van Dongen, J.J., Langerak, A.W., Schuurink, E.M., van Miquel, J.F., garzia Sanz, R., Parreira, A., Smith, J.L., Lavender, F.L., Morgan, G.J., Evans, P.A., Kneba, M., Hummel, M., Macintyre, E.A. and Bastard, C.
TITLE Nucleic acid amplification primers for PCR-based clonality studies
JOURNAL Patent: WO 2004033728-A 9 22-APR-2004;
Erasmus Universiteit Rotterdam (NL); Van Dongen, Jacobus, Johannes, Maria (NL)
FEATURES
source
1..39
Location/Qualifiers

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Description of Artificial Sequence: primer"

ORIGIN
Query Match          74.4%; Score 13.4; DB 6; Length 39;
Best Local Similarity 93.3%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCAAAGTGGCCGAG 17
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Db 32 TCAAAGGGGCCGAG 18

RESULT 4
AX206894/c
LOCUS AX206894 44 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 2 from Patent WO0155429.
ACCESSION AX206894
VERSION AX206894.1 GI:15394705
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Mattanovich,D., Katinger,H., Hohenblum,H., Naschberger,S. and Weik,R.
TITLE Method for the manufacture of recombinant trypsin
JOURNAL Patent: WO 0155429-A 2 02-AUG-2001;
POLYMER Scientific Immunobiologische Forschung GmbH (AT)
FEATURES
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="PCR primer"

ORIGIN
Query Match          74.4%; Score 13.4; DB 6; Length 44;
Best Local Similarity 93.3%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATCAAAGTGGCCG 15
    |||||
Db 38 CATCAAAGGGGCCG 24

RESULT 5
AX146612
LOCUS AX146612 45 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 74 from Patent WO0134654.
ACCESSION AX146612
VERSION AX146612.1 GI:14285005
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Strauch,K.
TITLE Hedgehog fusion proteins and uses
JOURNAL Patent: WO 0134654-A 74 17-MAY-2001;
BIOGEN, INC. (US)
FEATURES
    source
        1..45
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN
Query Match          74.4%; Score 13.4; DB 6; Length 45;
Best Local Similarity 93.3%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATCAAAGTGGCCG 15
    |||||
Db 38 CATCAAAGGGGCCG 24

RESULT 6
QY32654
LOCUS QY32654 65 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 2289 from Patent WO0210449.
ACCESSION QY32654
VERSION QY32654.1 GI:41498918
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
JOURNAL variants that populate a transcriptome
PATENT: WO 0210449-A 2289 07-FEB-2002;
Compugen Inc. (US)
FEATURES
    source
        1..65
            /organism="Rattus norvegicus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:10116"

ORIGIN
Query Match          74.4%; Score 13.4; DB 6; Length 65;
Best Local Similarity 93.3%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGTGGCCGAGA 18
    |||||
Db 26 CCAAGTGGCCGAGA 40

RESULT 7
CEL487557/c
LOCUS CEL487557 23 bp RNA linear INV 09-OCT-2003
DEFINITION Caenorhabditis elegans microRNA mir-2.
ACCESSION AJ487557
VERSION AJ487557.2 GI:35210303
KEYWORDS microRNA; mir-2 gene; miRNA.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1
AUTHORS Lau,N.C., Lim,L.P., Weinstein,E.G. and Bartel,D.P.
TITLE An abundant class of tiny RNAs with probable regulatory roles in
JOURNAL Caenorhabditis elegans
PUBMED Science 294 (5543), 858-862 (2001)
REFERENCE 2
AUTHORS Bartel,D.P.
TITLE Direct Submision
JOURNAL Submitted (25-MAR-2002) Bartel D.P., Biology, MIT and Whitehead
INSTITUTE, 9 Cambridge Center, Cambridge, MA, 02142, USA
REMARK revised by [3]
REFERENCE 3 (bases 1 to 23)
AUTHORS Bartel,D.P.
TITLE Direct Submision
JOURNAL Submitted (16-SEP-2003) Bartel D.P., Biology, MIT and Whitehead
INSTITUTE, 9 Cambridge Center, Cambridge, MA, 02142, USA
COMMENT On Sep 25, 2003 this sequence version replaced gi:21212795.
FEATURES
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/organism="Caenorhabditis elegans"
/mol_type="other RNA"
/db_xref="taxon:6239"
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1..23
1..23
/organism="Drosophila melanogaster"
/mol_type="other RNA"
/db_xref="taxon:7227"
/chrosome="2L"
/notes="transcribed as larger precursor, predicted form
hairpin"

gene
misc_RNA

ORIGIN
Query Match 73.3%; Score 13.2; DB 2; Length 23;
Best Local Similarity 83.3%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAGA 18
Db 20 CATCAAGGTGGCTGTGA 3

RESULT 8
DME421757/c
LOCUS DME421757 23 bp RNA linear INV 11-JUN-2003
DEFINITION Drosophila melanogaster microRNA mir-2a-1.
ACCESSION AJ421757
VERSION AJ421757.1 GI:17646042
KEYWORDS miRNA.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 23)
AUTHORS Lagos-Quintana,M., Rauhut,R., Lendeckel,W. and Tuschl,T.
TITLE Identification of novel genes coding for small expressed RNAs
JOURNAL Science 294 (5543), 853-858 (2001)
PUBMED 11679670
REFERENCE 2 (bases 1 to 23)
AUTHORS Tuschl,T.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-2001) Dep. of Cellular Biochemistry, Max Planck
Institute for Biophysical Chemistry, Am Fassberg 11, Goettingen
37077, Germany
COMMENT Related sequences: AE003663.
FEATURES
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/organism="Drosophila melanogaster"
/mol_type="other RNA"
/db_xref="taxon:7227"
/chrosome="2L"
/notes="transcribed as larger precursor from the mir-2a-1
gene, predicted to form hairpin"

misc_RNA

ORIGIN
Query Match 73.3%; Score 13.2; DB 2; Length 23;
Best Local Similarity 83.3%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAGA 18
Db 20 CATCAAGGTGGCTGTGA 3

RESULT 9
DME421758/c
LOCUS DME421758 23 bp RNA linear INV 11-JUN-2003
DEFINITION Drosophila melanogaster microRNA mir-2a-2.
ACCESSION AJ421758
VERSION AJ421758.1 GI:17646043
KEYWORDS miRNA.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 23)
AUTHORS Lagos-Quintana,M., Rauhut,R., Lendeckel,W. and Tuschl,T.
TITLE Identification of novel genes coding for small expressed RNAs
JOURNAL Science 294 (5543), 853-858 (2001)
PUBMED 11679670
REFERENCE 2 (bases 1 to 23)
AUTHORS Tuschl,T.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-2001) Dep. of Cellular Biochemistry, Max Planck
Institute for Biophysical Chemistry, Am Fassberg 11, Goettingen
37077, Germany
COMMENT Related sequences: AE003663.
FEATURES
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/organism="Drosophila melanogaster"
/mol_type="other RNA"
/db_xref="taxon:7227"
/chrosome="2L"
/notes="transcribed as larger precursor from the mir-2a-1
gene, predicted to form hairpin"

misc_RNA

ORIGIN
Query Match 73.3%; Score 13.2; DB 2; Length 23;
Best Local Similarity 83.3%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAGA 18
Db 20 CATCAAGGTGGCTGTGA 3

RESULT 10
Q0873596/c
LOCUS Q0873596 23 bp RNA linear PAT 27-SEP-2004
DEFINITION Sequence 15 from Patent WO2004076622.
ACCESSION Q0873596
VERSION Q0873596.1 GI:52747188
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Hominidae; Homo.
REFERENCE 1
AUTHORS Taira,K. and Kawasaki,H.
TITLE Regulation of mammalian cells
JOURNAL Patent: WO 2004076622-A 15 10-SEP-2004;
National Institute of Advanced Industrial Science and Technology
(JP)
FEATURES
source
1..23
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
/notes="transcribed as larger precursor from the mir-2a-2
gene, predicted to form hairpin"

misc_RNA

ORIGIN
Query Match 73.3%; Score 13.2; DB 6; Length 23;
Best Local Similarity 83.3%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAGA 18
Db 20 CATCAAGGTGGCTGTGA 3

RESULT 11
Q006930
LOCUS Q006930 51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 5570 from Patent WO0147944.

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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 23)
AUTHORS Lagos-Quintana,M., Rauhut,R., Lendeckel,W. and Tuschl,T.
TITLE Identification of novel genes coding for small expressed RNAs
JOURNAL Science 294 (5543), 853-858 (2001)
PUBMED 11679670
REFERENCE 2 (bases 1 to 23)
AUTHORS Tuschl,T.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-2001) Dep. of Cellular Biochemistry, Max Planck
Institute for Biophysical Chemistry, Am Fassberg 11, Goettingen
37077, Germany
COMMENT Related sequences: AE003663.
FEATURES
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/organism="Drosophila melanogaster"
/mol_type="other RNA"
/db_xref="taxon:7227"
/chrosome="2L"
/notes="transcribed as larger precursor from the mir-2a-2
gene, predicted to form hairpin"

misc_RNA

ORIGIN
Query Match 73.3%; Score 13.2; DB 2; Length 23;
Best Local Similarity 83.3%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAGA 18
Db 20 CATCAAGGTGGCTGTGA 3

RESULT 10
Q0873596/c
LOCUS Q0873596 23 bp RNA linear PAT 27-SEP-2004
DEFINITION Sequence 15 from Patent WO2004076622.
ACCESSION Q0873596
VERSION Q0873596.1 GI:52747188
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Hominidae; Homo.
REFERENCE 1
AUTHORS Taira,K. and Kawasaki,H.
TITLE Regulation of mammalian cells
JOURNAL Patent: WO 2004076622-A 15 10-SEP-2004;
National Institute of Advanced Industrial Science and Technology
(JP)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
/notes="transcribed as larger precursor from the mir-2a-2
gene, predicted to form hairpin"

misc_RNA

ORIGIN
Query Match 73.3%; Score 13.2; DB 6; Length 23;
Best Local Similarity 83.3%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAGA 18
Db 20 CATCAAGGTGGCTGTGA 3

RESULT 11
Q006930
LOCUS Q006930 51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 5570 from Patent WO0147944.

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ACCESSION      CQ006930
VERSION        CQ006930.1  GI:41013562
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.

REFERENCE      1
AUTHORS        Shimkets,R.A. and Leach,M.
TITLE          Nucleic acids containing single nucleotide polymorphisms and
               methods of use thereof
JOURNAL        Patent: WO 0147944-A 5570 05-JUL-2001;
               Curagen Corporation (US)
FEATURES       Location/Qualifiers
               source
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               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"
               /note="Accession number C943931116"

ORIGIN
Query Match      73.3%; Score 13.2; DB 6; Length 51;
Best Local Similarity 83.3%; Pred. No. 1.6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CATCAAGGTGCCGAGA 18
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Db      2 CAACAAGATGCCGTGA 19
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RESULT 12
AX233504/c
LOCUS          AX233504
DEFINITION     Sequence 147 from Patent WO0162788.
ACCESSION      AX233504
VERSION        AX233504.1  GI:15593016
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.

REFERENCE      1
AUTHORS        Olaveson,M., Lench,N., Allen,M. and Tazi-Ahmini,R.U.
TITLE          Corneodesmosin based test and model for inflammatory disease
JOURNAL        Patent: WO 0162788-A 147 30-AUG-2001;
               Oxagen Limited (GB)
FEATURES       Location/Qualifiers
               source
               1..68
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

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Query Match      73.3%; Score 13.2; DB 6; Length 68;
Best Local Similarity 83.3%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CATCAAGGTGCCGAGA 18
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Db      62 CATCCAGGTGCCGAGA 45
      ||||| ||||| |||||

RESULT 13
CQ874036/c
LOCUS          CQ874036
DEFINITION     Sequence 455 from Patent WO2004076622.
ACCESSION      CQ874036
VERSION        CQ874036.1  GI:52747628
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE      1
AUTHORS        Taiza,K. and Kawasaki,H.
TITLE          Regulation of mammalian cells
JOURNAL        Patent: WO 2004076622-A 455 10-SEP-2004;
               National Institute of Advanced Industrial Science and Tec hnology
               (JP)
FEATURES       Location/Qualifiers
               source
               1..76
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

ORIGIN
Query Match      73.3%; Score 13.2; DB 6; Length 76;
Best Local Similarity 83.3%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CATCAAGGTGCCGAGA 18
      ||||| ||||| |||||
Db      68 CATCAAGCTGGCTGTGA 51
      ||||| ||||| |||||

RESULT 14
S76293
LOCUS          Hox-A|Hox-1 {clone 29c} [rats, Sprague-Dawley, liver, Genomic, 80
               nt].
DEFINITION     S76293.1  GI:913078
ACCESSION      S76293
VERSION        S76293.1
KEYWORDS
SOURCE         Rattus sp.
ORGANISM       Rattus sp.
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE      1 (bases 1 to 80)
AUTHORS        Sakoyama,Y., Mizuta,I., Ogasawara,N. and Yoshikawa,H.
TITLE          Cloning of rat homeobox genes
JOURNAL        Biochem. Genet. 32 (9-10), 351-360 (1994)
PUBMED        7702549
REMARK        GenBank staff at the National Library of Medicine created this
               entry [NCBI gibbon 162650] from the original journal article.

FEATURES       Location/Qualifiers
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               1..80
               /organism="Rattus sp."
               /mol_type="genomic DNA"
               /db_xref="taxon:10118"
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               <21..>80
               /gene="Hox-A|Hox-1"
               /codon_start=1
               /product="Hox-1|Hox-A"
               /protein_id="AAP31865.1"
               /db_xref="GI:30352206"
               /translation="GKRARTAYTRYQTLEKEF"

ORIGIN
Query Match      73.3%; Score 13.2; DB 9; Length 80;
Best Local Similarity 83.3%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CATCAAGGTGCCGAGA 18
      ||||| ||||| |||||
Db      2 CAACATAGTGGCCGAGA 19
      ||||| ||||| |||||

RESULT 15
AR086069
LOCUS          AR086069
               18 bp DNA linear PAT 07-SEP-2000

```

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DEFINITION Sequence 53 from patent US 5985552.
ACCESSION AR086069
VERSION AR086069.1 GI:10012835
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Howell,M.D., Brostoff,S.W. and Carlo,D.J.
TITLE Vaccination and methods against diseases resulting from pathogenic
responses by specific T cell populations
JOURNAL Patent: US 5985552-A 53 16-NOV-1999;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 AAGGTGCCCGAGA 18
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Db 5 AAGGTGCCCGAGA 17
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RESULT 16
AR140423
LOCUS AR140423 18 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 53 from patent US 6207645.
ACCESSION AR140423
VERSION AR140423.1 GI:14482919
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Howell,M.D., Brostoff,S.W. and Carlo,D.J.
TITLE Vaccination and methods against diseases resulting from pathogenic
responses by specific T cell populations
JOURNAL Patent: US 6207645-A 53 27-MAR-2001;
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Db 5 AAGGTGCCCGAGA 17
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RESULT 17
AR146904
LOCUS AR146904 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 53 from patent US 6221352.
ACCESSION AR146904
VERSION AR146904.1 GI:15110707
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Howell,M.D., Brostoff,S.W. and Carlo,D.J.
TITLE Method of preventing the proliferation of v.beta.14 or
v.beta.17-Expressing T cells
JOURNAL Patent: US 6221352-A 53 24-APR-2001;
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Db 5 AAGGTGCCCGAGA 17
    |||||
RESULT 18
HSA403872
LOCUS HSA403872 33 bp mRNA linear PRI 24-MAY-2000
DEFINITION Homo sapiens partial mRNA for histone specific T-cell receptor beta
chain, D-J region, (TCRBJ2.1 gene).
ACCESSION AJ403872
VERSION AJ403872.1 GI:8217162
KEYWORDS Joining segment; T-cell receptor beta; TCR beta chain; TCRBJ2.1
Gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Andreassen,K., Bendiksen,S., Moens,U., Van Ghelue,M. and Rekvig,O.
TITLE Comparison of precursor frequencies and receptor structures of
histone specific T cells from SLE patients and from normal
individuals reveals no major differences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 33)
AUTHORS Andreassen,K.
TITLE Direct Submission
JOURNAL Submitted (03-MAY-2000) Andreassen K., Molecular Genetics, Medical
Biology, University of Tromsøe, Mh, 9037 Tromsøe, NORWAY
FEATURES
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Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 AAGGTGCCCGAGA 18
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Db 32 AAGGTGCCCGAGA 20
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RESULT 19
AX727459
LOCUS AX727459 17 bp DNA linear PAT 08-MAY-2003
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```

DEFINITION Sequence 5146 from Patent WO03025176.
ACCESSION AX727459
VERSION AX727459.1 GI:30506802
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 5146 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Best Local Similarity 87.5%; Pred. No. 2.4e+04;
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QY 2 ATCAAAGGTGGCGGAG 17
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Db 2 ATCAAACGTGGCTGAG 17
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RESULT 20
AR164017/c
LOCUS AR164017 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 216 from patent US 6271030.
ACCESSION AR164017
VERSION AR164017.1 GI:16234923
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1
AUTHORS Monia,B.P., Butler,M.M. and Wyatt,J.
TITLE Antisense inhibition of C/EBP beta expression
JOURNAL Patent: US 6271030-A 216 07-AUG-2001;
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Best Local Similarity 87.5%; Pred. No. 2.5e+04;
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|||||
Db 17 ATCAAACGTGGCTGAG 2
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RESULT 21
AX059371
LOCUS AX059371 20 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 104 from Patent WO0055325.
ACCESSION AX059371
VERSION AX059371.1 GI:12311476
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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JOURNAL
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Best Local Similarity 87.5%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 ATCAAAGGTGGCGGAG 17
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Db 4 ATCAAAGGGGGACGAG 19
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RESULT 22
CQ890713/c
LOCUS CQ890713 23 bp DNA linear PAT 01-NOV-2004
DEFINITION Sequence 56 from Patent EP1469072.
ACCESSION CQ890713
VERSION CQ890713.1 GI:55163634
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Barden,N., Sillaber,I. and Paez-Pereda,M.
TITLE Means and methods for diagnosing and treating affective disorders
JOURNAL Patent: EP 1469072-A 56 20-OCT-2004;
NeuroNova Aktiengesellschaft (DE)
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Best Local Similarity 87.5%; Pred. No. 2.5e+04;
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QY 2 ATCAAAGGTGGCGGAG 17
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Db 16 ATCAAAGCTGGACGAG 1
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RESULT 23
CQ897253/c
LOCUS CQ897253 23 bp DNA linear PAT 08-NOV-2004
DEFINITION Sequence 56 from Patent WO2004092384.
ACCESSION CQ897253
VERSION CQ897253.1 GI:55582073
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Hominidae; Homo.
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/db_xref="taxon:9606"
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Best Local Similarity 87.5%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 ATCAAAGGTGGCGGAG 17
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Db 16 ATCAAAGCTGGACGAG 1
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Job time : 378.932 secs

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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGGCCGAG 17
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Db 16 ATCAAGCTGGACGAG 1

RESULT 24
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LOCUS CQ898402 23 bp DNA linear PAT 08-NOV-2004
DEFINITION Sequence 56 from Patent EP1473367.
ACCESSION CQ898402
VERSION CQ898402.1 GI:55582721
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Barden, N., Sillaber, I. and Paetz-Pereda, M.
TITLE Means and methods for diagnosing and treating affective disorders
JOURNAL Patent: EP 1473367-A 56 03-NOV-2004;
NeuroNova Aktiengesellschaft (DE)
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Query Match 71.1%; Score 12.8; DB 6; Length 23;
Best Local Similarity 87.5%; Pred. No. 2.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGGCCGAG 17
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Db 16 ATCAAGCTGGACGAG 1

RESULT 25
AX206899/c
LOCUS AX206899 27 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 7 from Patent WO0155429.
ACCESSION AX206899
VERSION AX206899.1 GI:15394711
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Mattanovich, D., Katinger, H., Hohenblum, H., Naschberger, S. and Weisk, R.
TITLE Method for the manufacture of recombinant trypsin
JOURNAL Patent: WO 0155429-A 7 02-AUG-2001;
Polymun Scientific Immunobiologische Forschung GmbH (AT)
FEATURES
source 1..27
/organism="synthetic construct"
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/note="PCR primer"

ORIGIN

Query Match 71.1%; Score 12.8; DB 6; Length 27;
Best Local Similarity 87.5%; Pred. No. 2.6e+04;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:02:58 ; Search time 117.534 Seconds
(without alignments)
1020.680 Million cell updates/sec

Title: US-10-655-801-19

Perfect score: 18

Sequence: 1 catcaaggtgcccaga 18

Scoring table: IDENTITY NUC

Gapop 10.0 ; Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 5180220

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	100.0	18	Aa47975	Aa47975 Human ind
2	13.8	76.7	36	Adf16779	Adf16779 Human alb
3	13.8	76.7	36	Adf16777	Adf16777 Human alb
4	13.8	76.7	47	Aa063832	Aa063832 Oligonuc
5	13.4	74.4	39	Adm94051	Adm94051 Rearrange
6	13.4	74.4	44	AAD11004	AAD11004 Human oli
7	13.4	74.4	45	AAD09077	AAD09077 Human try
8	13.4	74.4	63	Abz76323	Abz76323 Plasmid p
9	13.4	74.4	65	Abn29541	Abn29541 Rat splic
10	13.2	73.3	22	Abz79786	Abz79786 Drosophil
11	13.2	73.3	22	Abz79480	Abz79480 Drosophil
12	13.2	73.3	22	Abz79324	Abz79324 Caenorhab
13	13.2	73.3	22	Abz79630	Abz79630 Caenorhab
14	13.2	73.3	23	Ada00062	Ada00062 D. melano
15	13.2	73.3	23	Adz83113	Adz83113 Human mir
16	13.2	73.3	23	Adw06866	Adw06866 siRNA ant
17	13.2	73.3	23	Ady31025	Ady31025 Micro RNA
18	13.2	73.3	23	Ady31024	Ady31024 Micro RNA
19	13.2	73.3	42	Adf16111	Adf16111 Human alb

20	13.2	73.3	51	4	AAL32362	Aal32362 Human SNP
21	13.2	73.3	68	5	AAS43685	Aas43685 Corneodes
22	13.2	73.3	72	9	ADA37054	Ada37054 Sim-2-CTL
23	13.2	73.3	76	13	ACF04460	Acf04460 Biomolecu
24	13.2	73.3	76	13	ADR83553	Adr83553 Human DNA
25	13	72.2	18	2	AAQ27315	AaQ27315 PCR prime
26	13	72.2	18	2	AAQ46299	AaQ46299 Primer Cb
27	13	72.2	18	2	AAQ96135	AaQ96135 Human C-b
28	13	72.2	18	2	AAV64293	Aav64293 Human T c
29	13	72.2	18	4	AAF85281	Aaf85281 PCR prime
30	13	72.2	18	5	AAF27154	Aaf27154 Human TCR
31	12.8	71.1	17	8	ACC67899	Acc67899 Murine ol
32	12.8	71.1	17	8	ACC67899	Acc67899 Murine ol
33	12.8	71.1	20	3	AAF22198	Aaf22198 Arabidops
34	12.8	71.1	21	13	ADU31111	AdU31111 Knock-dow
35	12.8	71.1	21	13	ADU25987	AdU25987 p2X7R ion
36	12.8	71.1	23	13	ADU23814	AdU23814 Human ATP
37	12.8	71.1	25	9	AC114729	Ac114729 Human mic
38	12.8	71.1	26	14	ADM75569	Adm75569 Epstein B
39	12.8	71.1	26	5	AAS22050	Aas22050 Human COL
40	12.8	71.1	27	4	AAD11009	Aad11009 Human try
41	12.8	71.1	29	3	AAZ33403	Aaz33403 Human try
42	12.8	71.1	37	2	AAT36734	Aat36734 Rat vasop
43	12.8	71.1	38	2	AAQ63831	AaQ63831 Oligonuc
44	12.8	71.1	42	14	ABE11187	Aeb11187 Mutagenes
45	12.8	71.1	52	2	AAQ31788	AaQ31788 Primer KS
46	12.8	71.1	57	14	ADY21518	AdY21518 Anti-CD37
47	12.8	71.1	60	6	ABN50725	Abn50725 Human spl
48	12.8	71.1	60	14	ADY21591	AdY21591 Antibody
49	12.8	71.1	60	14	ADY21589	AdY21589 Antibody
50	12.8	71.1	65	6	ABN51818	Abn51818 Mouse spl
51	12.8	71.1	65	6	ABN27922	Abn27922 Rat splic
52	12.8	71.1	65	6	ABN53195	Abn53195 Mouse spl
53	12.8	71.1	65	6	ABN31403	Abn31403 Rat splic
54	12.8	71.1	74	14	ABE50316	Aeb50316 Human cal
55	12.8	71.1	75	14	AEAS4972	Aeas4972 m22(iscfv)
56	12.4	68.9	18	4	AAS13755	Aas13755 Simple se
57	12.4	68.9	19	3	AaA83288	AaA83288 cdk8 ribo
58	12.4	68.9	19	5	AaH58450	AaH58450 Cell-cycl
59	12.4	68.9	20	6	ADP39686	Adp39686 Human GPx
60	12.4	68.9	20	6	ABL50080	AbL50080 Detergent
61	12.4	68.9	20	10	ABZ87053	Abz87053 Human oli
62	12.4	68.9	20	11	ABD23283	Abd23283 Human myo
63	12.4	68.9	24	3	AAC87764	Aac87764 SNORF36 r
64	12.4	68.9	24	3	AAC87788	Aac87788 Human SNO
65	12.4	68.9	24	4	AAF76353	Aaf76353 Human kIo
66	12.4	68.9	26	12	ADP12402	Adp12402 Taqman pr
67	12.4	68.9	29	3	AAA23981	Aaa23981 Oestrogen
68	12.4	68.9	32	4	AAD11008	Aad11008 Human try
69	12.4	68.9	33	12	ADK60398	Adk60398 Angiogene
70	12.4	68.9	33	12	ADK60699	Adk60699 Angiogene
71	12.4	68.9	33	12	ADP73322	Adp73322 Primer of
72	12.4	68.9	37	3	AAA50913	Aaa50913 Human CD4
73	12.4	68.9	40	14	ADM78469	Adm78469 Hybridiz
74	12.4	68.9	45	3	AAC87758	Aac87758 SNORF36 r
75	12.4	68.9	50	2	AAQ93217	AaQ93217 Primer CS
76	12.4	68.9	50	6	ABZ04067	Abz04067 Human leu
77	12.4	68.9	51	4	AAL26947	Aal26947 Human SNP
78	12.4	68.9	51	4	AAL31431	Aal31431 Human SNP
79	12.4	68.9	60	6	ABN34848	Abn34848 EGFR inh
80	12.4	68.9	77	14	ADM26288	Adm26288 EGFR inh
81	12.2	67.8	20	3	AAS58240	Aas58240 Mouse gly
82	12.2	67.8	20	3	AAZ5584	Aaz5584 Uteroglob
83	12.2	67.8	20	6	ABL57690	AbL57690 Human Gap
84	12.2	67.8	20	6	ABZ15349	Abz15349 Glyceral
85	12.2	67.8	20	8	ABZ74935	Abz74935 Mouse acy
86	12.2	67.8	20	10	ABZ97862	Abz97862 Human sot
87	12.2	67.8	20	10	ABV75849	Abv75849 Human gly
88	12.2	67.8	20	11	ABD30893	Abd30893 Human sot
89	12.2	67.8	20	12	ADK94860	Adk94860 Primer of
90	12.2	67.8	20	12	ADJ59737	Adj59737 Oligonuc
91	12.2	67.8	20	12	ADO45227	Ado45227 Human oli
92	12.2	67.8	20	13	ADS00468	AdS00468 Human GAD

93 12.2 67.8 20 14 ADZ80653 PCR prime
94 12.2 67.8 20 14 ADZ71209 Human GAP
95 12.2 67.8 20 14 AEB22289
c 96 12.2 67.8 21 6 ABA03932 Plasmodiu
c 97 12.2 67.8 21 10 ADJ95309 Human pre
c 98 12.2 67.8 21 12 ADL65387
c 99 12.2 67.8 21 12 ADL27554 PCR prime
c 100 12.2 67.8 22 6 ABK15251 Corn nk60

ALIGNMENTS

RESULT 1
AAH47975
ID AAH47975 standard; DNA; 18 BP.
XX
AC AAH47975;
XX
XX 02-OCT-2001 (first entry)
XX
XX Human inducible NOS antisense oligonucleotide SEQ ID NO 19.
XX
XX Antisense oligonucleotide; inducible nitric oxide synthase; NOS;
KW modulate expression; immunomodulator; antidiabetic; cardiovascular;
KW cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;
KW 2'-O-methoxyethyl; phosphorothioate; human; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
PH modified_base 1..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone, 5' and 3' four
FT nucleotide 2'-MOE (2'-O-methoxyethyl) wings (the cytidine
FT residues in the 2'-MOE wings are 5-methylcytidines) and a
FT deoxy gap"
XX
XX WO200152902-A1.
XX
XX 26-JUL-2001.
XX
XX 15-JAN-2001; 2001WO-US001381.
XX
XX 24-JAN-2000; 2000US-00490208.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Dean NM, Cowser LM;
PI
XX WPI; 2001-465340/50.
XX
XX New antisense oligonucleotides for modulating the expression of inducible
PT nitric oxide synthase in cells or tissues, particularly useful for
PT treating e.g. immunological, cardiovascular or neurological disorders, or
PT ischaemia.
XX
XX Claim 3; Page 83; 144pp; English.
XX
XX The invention relates to antisense compounds, especially
CC oligonucleotides, which are targeted to a nucleic acid encoding inducible
CC nitric oxide synthase and which specifically hybridise to and modulate
CC expression of inducible nitric oxide synthase. The antisense compounds
CC have immunomodulator, antidiabetic, cardiovascular, cardiant,
CC neuroprotective, disorder and vasotropic activity. The antisense
CC oligonucleotides are useful for inhibiting the expression of inducible
CC nitric oxide synthase in cells or tissues. In particular, the antisense
CC oligonucleotides are useful for treating diseases or disorders associated
CC with inducible nitric oxide synthase, e.g. diabetes, immunological
CC disorder, cardiovascular disorder, neurological disorder or
CC ischaemia/reperfusion injury. The antisense oligonucleotides are also
CC useful for research and diagnostics. The present sequence is that of an

CC antisense 2'-O-methoxyethyl gapmer oligonucleotide with a
CC phosphorothioate backbone, a central "gap" region of ten nucleotides
CC flanked by four nucleotide 2'-MOE (2'-methoxyethyl) wings (cytidine
CC residues in the 2'-MOE wings are 5-methylcytidines) and targeted to human
CC inducible nitric oxide synthase (NOS) mRNA (AAH47959)
XX
SQ Sequence 18 BP; 6 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAGA 18
Db 1 CATCAAGGTGGCCGAGA 18
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RESULT 2
ADF16779
ID ADF16779 standard; DNA; 36 BP.
XX
AC ADF16779;
XX
XX 12-FEB-2004 (first entry)
XX
DE Human albumin fusion protein-related PCR primer SeqID1957.
XX
KW albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy; diabetes mellitus; human; PCR; primer; ss.
XX
OS Homo sapiens.
XX
XX WO2003060071-A2.
XX
XX 24-JUL-2003.
XX
XX 23-DEC-2002; 2002WO-US040891.
XX
XX 21-DEC-2001; 2001US-0341811P.
XX 24-JAN-2002; 2002US-0350358P.
XX 28-JAN-2002; 2002US-0351360P.
XX 26-FEB-2002; 2002US-0359370P.
XX 28-FEB-2002; 2002US-0360000P.
XX 27-MAR-2002; 2002US-0367500P.
XX 08-APR-2002; 2002US-0370227P.
XX 10-MAY-2002; 2002US-0378950P.
XX 24-MAY-2002; 2002US-0382617P.
XX 28-MAY-2002; 2002US-0383123P.
XX 05-JUN-2002; 2002US-0385708P.
XX 10-JUL-2002; 2002US-0394625P.
XX 24-JUL-2002; 2002US-0398008P.
XX 09-AUG-2002; 2002US-0402131P.
XX 13-AUG-2002; 2002US-0402708P.
XX 18-SEP-2002; 2002US-0411355P.
XX 18-SEP-2002; 2002US-0411426P.
XX 02-OCT-2002; 2002US-0414984P.
XX 11-OCT-2002; 2002US-0417611P.
XX 23-OCT-2002; 2002US-0420246P.
XX 05-NOV-2002; 2002US-0423623P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (DELZ) DELTA BIOTECHNOLOGY LTD.
XX (PRIN-) PRINCIPIA PHARM CORP.
XX
XX Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
PI
XX WPI; 2003-598517/56.
XX
XX New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.
XX
XX Example 4; SEQ ID NO 1957; 24pp; English.
PS

XX This invention relates to a novel albumin fusion protein having albumin
 CC or biological activity. Human serum albumin is responsible for a
 CC significant proportion of the osmotic pressure of serum and also
 CC functions as a carrier of endogenous and exogenous ligands. The fusion of
 CC albumin to a therapeutic protein may increase shelf-life and stability of
 CC the therapeutic protein. The albumin fusion protein of the invention may
 CC allow production of compositions with antidiabetic activity whilst the
 CC nucleotide sequence which encodes it may be useful for gene therapy. The
 CC albumin fusion protein is useful for preparing a composition for treating
 CC diabetes mellitus. The present sequence is that of a PCR primer which may
 CC be used for amplification of a DNA sequence encoding a therapeutic
 CC protein which was fused with human albumin to create a novel albumin
 CC fusion protein of the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/publishedpct_sequences
 XX
 SQ Sequence 36 BP; 8 A; 8 C; 13 G; 7 T; 0 U; 0 Other;
 Query Match 76.7%; Score 13.8; DB 10; Length 36;
 Best Local Similarity 88.2%; Pred. No. 2.3e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 ATCAAGGTGGCGGAGA 18
 Db |||||
 15 ATCAAGGTGGCGGTAGA 31
 RESULT 3
 ADF16777
 ID ADF16777 standard; DNA; 36 BP.
 AC ADF16777;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human albumin fusion protein-related PCR primer SeqID1955.
 XX
 KW albumin fusion protein; albumin activity; human serum albumin;
 KW serum osmotic pressure; shelf-life; stability; antidiabetic;
 KW gene therapy; diabetes mellitus; human; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003060071-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 23-DEC-2002; 2002WO-US040891.
 XX
 PR 21-DEC-2001; 2001US-0341811P.
 PR 24-JAN-2002; 2002US-0350358P.
 PR 28-JAN-2002; 2002US-0351360P.
 PR 26-FEB-2002; 2002US-0359370P.
 PR 28-FEB-2002; 2002US-0360000P.
 PR 27-MAR-2002; 2002US-0367500P.
 PR 08-APR-2002; 2002US-0370227P.
 PR 10-MAY-2002; 2002US-0378950P.
 PR 24-MAY-2002; 2002US-0382617P.
 PR 28-MAY-2002; 2002US-0383123P.
 PR 05-JUN-2002; 2002US-0385708P.
 PR 10-JUL-2002; 2002US-0394625P.
 PR 24-JUL-2002; 2002US-0398008P.
 PR 09-AUG-2002; 2002US-0402131P.
 PR 13-AUG-2002; 2002US-0402708P.
 PR 18-SEP-2002; 2002US-0411355P.
 PR 18-SEP-2002; 2002US-0411426P.
 PR 02-OCT-2002; 2002US-0414984P.
 PR 11-OCT-2002; 2002US-0417611P.
 PR 23-OCT-2002; 2002US-0420246P.
 PR 05-NOV-2002; 2002US-0423623P.
 XX

PA (HUMA-) HUMAN GENOME SCI INC.
 PA (DELZ) DELTA BIOTECHNOLOGY LTD.
 PA (PRIN-) PRINCIPIA PHARM CORP.
 XX
 PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
 XX WPI; 2003-598517/56.
 DR
 XX New albumin fusion protein, useful for preparing a composition for
 PT treating diabetes mellitus.
 XX
 PS Example 4; SEQ ID NO 1955; 24pp; English.
 XX
 CC This invention relates to a novel albumin fusion protein having albumin
 CC or biological activity. Human serum albumin is responsible for a
 CC significant proportion of the osmotic pressure of serum and also
 CC functions as a carrier of endogenous and exogenous ligands. The fusion of
 CC albumin to a therapeutic protein may increase shelf-life and stability of
 CC the therapeutic protein. The albumin fusion protein of the invention may
 CC allow production of compositions with antidiabetic activity whilst the
 CC nucleotide sequence which encodes it may be useful for gene therapy. The
 CC albumin fusion protein is useful for preparing a composition for treating
 CC diabetes mellitus. The present sequence is that of a PCR primer which may
 CC be used for amplification of a DNA sequence encoding a therapeutic
 CC protein which was fused with human albumin to create a novel albumin
 CC fusion protein of the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/publishedpct_sequences
 XX
 SQ Sequence 36 BP; 8 A; 8 C; 13 G; 7 T; 0 U; 0 Other;
 Query Match 76.7%; Score 13.8; DB 10; Length 36;
 Best Local Similarity 88.2%; Pred. No. 2.3e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 ATCAAGGTGGCGGAGA 18
 Db |||||
 15 ATCAAGGTGGCGGTAGA 31
 RESULT 4
 AAQ63832/c
 ID AAQ63832 standard; DNA; 47 BP.
 XX
 AC AAQ63832;
 XX
 DT 07-FEB-1995 (first entry)
 XX
 DE Oligonucleotide IKGR, used in construction of modified t-PA.
 XX
 KW Tissue plasminogen activator; t-PA; modified; variant;
 KW plasmin cleavage recognition site; C-terminal peptide; systemic bleeding;
 KW decrease; reduce; thrombosis treatment; anti-thrombotic; ss.
 XX
 OS Synthetic.
 XX
 PN JP06133780-A.
 XX
 PD 17-MAY-1994.
 XX
 PF 23-OCT-1992; 92JP-00309285.
 XX
 PR 23-OCT-1992; 92JP-00309285.
 XX
 PA (SUMU) SUMITOMO SEIYAKU KK.
 XX
 DR WPI; 1994-196164/24.
 XX
 PT New modified tissue plasminogen activator - comprises sequence which is
 PT recognised and cleaved by plasmin.
 XX
 PS Example 2; Page 8; 10pp; Japanese.

XX Oligonucleotide pairs DC and DCR, DO and DOR, and IKGG and IKGR (see
CC AAQ63827-063832) are annealed to produce 3 double-stranded fragments. The
CC fragments are ligated together to produce a fragment which can be
CC amplified by the polymerase chain reaction using oligonucleotides DC and
CC IKGR as primers. The amplified fragment was digested with BstEII and
CC SalI and the resulting fragment was used in the construction of plasmid
CC pUC-D01. The plasmid codes for a modified t-PA with a plasmin cleavage
CC site at its C-terminal end
XX

SQ Sequence 47 BP; 8 A; 13 C; 12 G; 14 T; 0 U; 0 Other;

Query Match 76.7%; Score 13.8; DB 2; Length 47;
Best Local Similarity 88.2%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAG 17
|||||
Db 39 CATCAAGGAGCCCTAG 23

RESULT 5

ADM94051/c
ID ADM94051 standard; DNA; 39 BP.

XX AC ADM94051;

XX DT 15-JUL-2004 (first entry)

XX DE Rearranged Ig and TCR gene related nucleotide.

XX DE nucleic acid amplification; primer; PCR; detection;

XX KW chromosomal translocation; human; clonal rearrangement;

XX KW chromosome aberration; lymphoproliferative disorder; Ig; TCR; gene; ds.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200403728-A2.

XX PD 22-APR-2004.

XX PF 13-OCT-2003; 2003WO-NL000690.

XX PR 11-OCT-2002; 2002US-0417779P.

XX PA (UYRO-) UNIV ROTTERDAM ERASMUS.

XX PA (DAVI/) DAVI F B L.

XX PI Van Dongen JJM, Langerak AW, Schuurink EMD, San Miquel JF;

XX PI Garzia Sanz R, Parreira A, Smith JL, Lavender FL, Morgan GJ;

XX PI Evans PAS, Kneba M, Hummel M, Macintyre EA, Bastard C;

XX DR WPI; 2004-364878/34.

XX PT New set of nucleic amplification primers comprising a forward primer and
XX a reverse primer and capable of amplifying a rearrangement, useful in
XX diagnosing lymphoproliferative disorders.

XX PS Disclosure; Fig 2; 121pp; English.

XX The present invention describes a set of nucleic amplification primers
CC capable of amplifying a VH-JH or DH-JH IGH, VK-JK or VK/intron-Kde IGH,
CC Vlambda-Jlambda IGL, Vbeta-Jbeta TCRB or Dbeta-Jbeta TCRB, VI-JY TCRG,
CC Vdelta-Jdelta, Ddelta-Ddelta or Vdelta-Ddelta TCRD rearrangement
CC comprises a forward primer and a reverse primer. Also described: (1) a
CC nucleic acid amplification assay, preferably a PCR or multiplex PCR
CC assay using the set of primers; (2) detecting VH-JH or DH-JH IGH, VK-JK
CC or VK/intron-Kde IGH, Vlambda-Jlambda IGL, Vbeta-Jbeta TCRB or Dbeta-
CC Jbeta TCRB, VI-JY TCRG, Vdelta-Jdelta, Ddelta-Ddelta or Vdelta-Ddelta
CC TCRD rearrangement; (3) detecting chromosomal translocation (11;14)(BCLg-
CC JG2-1) or t(14;18)(BCL2-IGH); (4) detecting human TBXAS1, recombination
CC activating protein (RAG1), promyelocytic leukaemia zinc finger protein

CC (PLZF) or AP4 gene; (5) assessing clonal rearrangements and/or chromosome
CC aberrations; and (6) a kit for the detecting at least one rearrangement
CC comprising the set of primers. The new set of nucleic amplification
CC primers capable of amplifying a VH-JH or DH-JH IGH, VK-JK or VK/intron-
CC Kde IGH, Vlambda-Jlambda IGL, Vbeta-Jbeta TCRB or Dbeta-Jbeta TCRB, VI-JY
CC TCRG, Vdelta-Jdelta, Ddelta-Ddelta or Vdelta-Ddelta TCRD rearrangement
CC are useful in diagnosing lymphoproliferative disorders. The present
CC sequence is used in the exemplification of the present invention.

XX

SQ Sequence 39 BP; 7 A; 13 C; 11 G; 8 T; 0 U; 0 Other;

Query Match 74.4%; Score 13.4; DB 12; Length 39;
Best Local Similarity 93.3%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TCAAAGGTGGCCGAG 17
|||||
Db 32 TCAAAGGGGGCCGAG 18

RESULT 6

AAD11004/c

ID AAD11004 standard; DNA; 44 BP.

XX AC AAD11004;

XX DT 24-SEP-2001 (first entry)

XX DE Human trypsinogen 1 gene cloning forward PCR primer #1.

XX DE Human; trypsinogen 1; trypsin; protein refolding; inclusion body;

XX KW pICZalpaB plasmid; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200155429-A2.

XX PD 02-AUG-2001.

XX PF 24-JAN-2001; 2001WO-EP000770.

XX PR 24-JAN-2000; 2000US-0177348P.

XX PA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.

XX PI Mattanovich D, Katinger H, Hohenblum H, Naschberger S, Weik R;

XX DR WPI; 2001-457733/49.

XX PT Recombinant manufacture of trypsin, comprises transforming a host cell,
XX incubating the transformed cells, and separating and optionally
XX processing the trypsinogen.

XX PS Example 1; Page 9; 22pp; English.

XX The invention relates to a method for the manufacture and purification of
CC recombinant trypsinogen and trypsin in E. coli and yeast, using high
CC yield expression vectors with and without secretion leader sequences. The
CC invention also relates to an improved method and apparatus for carrying
CC out protein refolding specifically useful for processing trypsinogen that
CC has accumulated intracellularly in the form of inclusion bodies. The
CC present DNA sequence is a forward PCR primer which is used for cloning
CC human trypsinogen 1 gene into the pICZalpaB plasmid. The PCR primer is
CC also used for expressing human trypsinogen 1 in the yeast Pichia pastoris

XX

SQ Sequence 44 BP; 7 A; 16 C; 12 G; 9 T; 0 U; 0 Other;

Query Match 74.4%; Score 13.4; DB 4; Length 44;

Best Local Similarity 93.3%; Pred. No. 3.9e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCG 15
|||||

```
Db 38 CATCAAGGGCGCG 24

RESULT 7
AAD09077
ID AAD09077 standard; DNA; 45 BP.
XX
AC AAD09077;
XX
XX
DT 04-SEP-2001 (first entry)
XX
DE Human oligonucleotide HOG-799 used to construct pMWC22.
XX
XX Human; hedgehog protein; neurotropic; neuroprotective; anticonvulsant;
XX cytoskeletal; therapy; Alzheimer's disease; Parkinson's disease; injury;
XX Huntington's chorea; amyotrophic lateral sclerosis; multiple sclerosis;
XX nervous system aging; neurodegenerative disease; immunological disease;
XX malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
XX extracellular signalling protein; HOG-799; ss.
XX
OS Homo sapiens.
XX
XX WO200134654-A1.
XX
XX 17-MAY-2001.
XX
XX 02-NOV-2000; 2000WO-US030405.
XX
XX 05-NOV-1999; 99US-0164025P.
XX
XX (BIOJ ) BIOGEN INC.
XX
XX Strauch K;
XX
XX WPI; 2001-329075/34.
XX
XX Novel isolated hedgehog fusion polypeptide useful for treating
XX neurological conditions such as Alzheimer's disease, Parkinson's disease,
XX Huntington's chorea, amyotrophic lateral sclerosis, and multiple
XX sclerosis.
XX
XX Example 1; Page 62; 178pp; English.
XX
XX The present invention relates to hedgehog fusion proteins. Hedgehog
XX proteins are a family of extracellular signalling proteins that regulate
XX various aspects of embryonic development both in vertebrates and in
XX invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
XX treatment of any condition or disease state for which a hedgehog or
XX patched protein constituent is efficacious and in the diagnosis of
XX constituents or conditions of disease states in biological system or
XX specimens and for diagnostic purposes in non-physiological systems.
XX Hedgehog fusion protein is useful for treating neurological conditions
XX due to injury, aging of nervous system, including Alzheimer's disease,
XX chronic neurodegenerative diseases of the nervous system, including
XX Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis
XX and chronic immunological diseases of nervous system including multiple
XX sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
XX tumours and to specifically target medical therapies against cancers and
XX tumours which express the receptor for the protein. The present sequence
XX is human oligonucleotide HOG-799 used to construct pMWC22, pMWC23, pMWC25
XX and pMWC26 plasmids which are used in the invention
XX
XX Sequence 45 BP; 12 A; 14 C; 10 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 74.4%; Score 13.4; DB 4; Length 45;
XX Best Local Similarity 93.3%; Pred. No. 3.9e+03;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 4 CAAAGGTGGCGGAGA 18
XX
XX 26 CCAAGGTGGCGGAGA 40
XX
Db

Db 38 CATCAAGGGCGCG 24

RESULT 8
ABZ76323/c
ID ABZ76323 standard; DNA; 63 BP.
XX
XX ABZ76323;
XX
XX
DT 12-JUN-2003 (first entry)
XX
DE Plasmid pIGT3 constructing antisense primer P4.
XX
XX Helper phage; Ex-phage; phagemid vector; coat protein; mutant;
XX phage display; PCR; primer; ss.
XX
XX Synthetic.
XX
XX WO2003018785-A1.
XX
XX 06-MAR-2003.
XX
XX 28-MAY-2002; 2002WO-KR001001.
XX
XX 29-AUG-2001; 2001KR-00052451.
XX
XX (IGTH-) IG THERAPY CO LTD.
XX
XX Cha S;
XX
XX WPI; 2003-300730/29.
XX
XX New mutant helper phage, termed Ex-phage, useful for packaging a phagemid
XX vector, isolating antibody molecules in phage display, or probing
XX candidate molecules for the development of therapeutic antibody drugs.
XX
XX Example 2; Page 50; 54pp; English.
XX
XX The invention relates to a mutant helper phage, termed Ex-phage, for
XX packaging a phagemid vector containing filamentous virus genome of which
XX at least a part of the gene of wild-type minor coat protein is deleted or
XX defective. Conditional suppressive translation stop codon is introduced
XX at the N-terminal of the gene of minor coat protein of the mutant helper
XX phage. The mutant helper phage is useful for packaging a phagemid vector,
XX isolating an antibody and selecting a recombinant virus expressing in
XX antibodies. The method is useful for isolating antibody molecules in
XX phage display, or increasing display level of foreign polypeptides on the
XX surface of recombinant phage in phage display technology. The phage
XX display library can be used at probing candidate molecules for the
XX development of therapeutic antibody drugs. Sequences ABZ76322-324
XX represent PCR primers used in the construction of a plasmid pIGT3
XX
XX Sequence 63 BP; 6 A; 18 C; 14 G; 25 T; 0 U; 0 Other;
XX
XX Query Match 74.4%; Score 13.4; DB 8; Length 63;
XX Best Local Similarity 93.3%; Pred. No. 4.1e+03;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 2 ATCAAGGTGGCGGA 16
XX
XX 48 ATCAAGGTGGCGGA 34
XX
Db

RESULT 9
ABN29541
ID ABN29541 standard; DNA; 65 BP.
XX
XX AC ABN29541;
XX
XX
DT 15-JUL-2002 (first entry)
XX
DE Rat spliced transcript detection oligonucleotide SEQ ID NO:2289.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
XX
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OS Rattus norvegicus.
XX WO200210449-A2.
XX 07-FEB-2002.
XX 20-JUL-2001; 2001WO-IB001903.
XX 28-JUL-2000; 2000US-0221607P.
XX 02-MAY-2001; 2001US-0287724P.
XX (COMP-) COMPUGEN INC.
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
PS Example 1; SEQ ID NO 2289; 47bp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC )transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridizing selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 65 BP; 16 A; 15 C; 18 G; 16 T; 0 U; 0 Other;

Query Match 74.4%; Score 13.4; DB 6; Length 65;
Best Local Similarity 93.3%; Pred. No. 4.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAGAAGTGGCCGAGA 18
DB 2 CAAGAAGTGGCCGAGA 16
|||||
RESULT 10
AEB79786
ID AEB79786 standard; RNA; 22 BP.
XX
XX AEB79786;
AC
XX
XX 20-OCT-2005 (first entry)
DT
XX
XX Drosophila melanogaster dme-miR-2c-targeted anti-microRNA, SEQ:610.
XX
XX RNA interference; gene silencing; anti-microRNA; anti-miRNA;
XX microRNA inhibitor; miRNA inhibitor; gene expression; gene regulation;
XX ss.
XX

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```

OS Drosophila melanogaster.
XX US2005182005-A1.
XX 19-AUG-2005.
XX 13-MAY-2004; 2004US-00845057.
XX 13-FEB-2004; 2004US-00778908.
XX (TUSC/) TUSCHL T H.
XX (LAND/) LANDTHALER M.
XX (WEIS/) MEISTER G.
XX (PFEF/) PFEFFER S.
XX Tuschl TH, Landthaler M, Meister G, Pfeiffer S;
XX WPI; 2005-554283/56.
XX
XX New isolated single stranded anti-microRNA molecule comprising a minimum
PT of ten moieties and a maximum of fifty moieties on a molecular backbone,
PT useful for inhibiting micro ribonucleoprotein particle (microRNP)
PT activity in a cell.
XX
PS Claim 1; SEQ ID NO 610; 115pp; English.
XX
XX The invention relates to isolated single-stranded anti-microRNA molecules
CC capable of inhibiting microRNP (microribonucleoprotein) activity. The
CC anti-microRNAs are: a) 10-50 bases in length; b) comprise unmodified or
CC modified ribonucleotides; c) comprise a region of at least 10 contiguous
CC bases identical to a portion of one of the human, mouse, rat, Drosophila
CC or Caenorhabditis elegans anti-microRNAs shown in AEB79483-AEB79788,
CC except that up to 30% of the bases are wobble bases, up to 10% of the
CC contiguous bases may be insertions, deletions, mismatches or combinations
CC thereof, and no more than 50% of these contiguous bases have
CC deoxyribonucleotide backbones; and d) have a mismatch with the base at
CC position 11 of the target microRNA. The invention also relates to a
CC method of inhibiting microRNP activity in a cell using the anti-microRNAs
CC of the invention, especially a human, mouse, rat, Drosophila or
CC Caenorhabditis elegans anti-microRNA. The invention further relates to
CC isolated microRNA molecules modified for increased nuclease resistance
CC which are: i) 10-50 bases in length; and ii) comprise at least 10
CC contiguous bases identical to one of the human, mouse, rat, Drosophila or
CC Caenorhabditis elegans microRNAs shown in AEB79177-AEB79314 and AEB79321-
CC AEB79482, except that up to 30% of the bases are wobble bases, up to 10%
CC of the contiguous bases may be insertions, deletions, mismatches or
CC combinations thereof, and no more than 50% of these contiguous bases have
CC deoxyribonucleotide backbones. Preferably, these microRNAs comprise an
CC inserted or deleted base or a base substitution at position 11. The anti-
CC microRNAs and microRNAs of the invention are useful for modulating gene
CC expression. As a component of animal microRNPs, microRNAs guide RNA
CC degradation in a similar way to short interfering RNA (siRNA)-induced
CC silencing complexes. Such microRNAs may be beneficial or harmful to cell
CC survival. If a particular microRNA is known to be beneficial, an
CC appropriate isolated microRNA of the invention may be introduced into a
CC cell to promote survival. Conversely, if a particular microRNA is known
CC to be harmful (e.g., one known to induce apoptosis or induce cancer),
CC then an appropriate anti-microRNA of the invention can be introduced into
CC a cell to inhibit microRNA activity. Additionally, the anti-microRNAs or
CC microRNAs of the invention may be introduced into a cell to study the
CC function of the microRNA. Sequences AEB79733-AEB79788 represent
CC specifically claimed Drosophila microRNA-directed anti-microRNAs upon
CC which anti-microRNAs of the invention may be based.
XX
SQ Sequence 22 BP; 6 A; 6 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 14; Length 22;
Best Local Similarity 72.2%; Pred. No. 4.6e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAGA 18
DB 3 CAUCAAAAGTGGCUGUGA 20
|||||

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CC contiguous bases identical to one of the human, mouse, rat, Drosophila or
 CC Caenorhabditis elegans microRNAs shown in AEB79177-AEB79314 and AEB79321-
 CC AEB79482, except that up to 30% of the bases are wobble bases, up to 10%
 CC of the contiguous bases may be insertions, deletions, mismatches or
 CC combinations thereof, and no more than 50% of these contiguous bases have
 CC deoxyribonucleotide backbones. Preferably, these microRNAs comprise an
 CC inserted or deleted base or a base substitution at position 11. The anti-
 CC microRNAs and microRNAs of the invention are useful for modulating gene
 CC expression. As a component of animal microRNPs, microRNAs guide RNA
 CC degradation in a similar way to short interfering RNA (siRNA)-induced
 CC silencing complexes. Such microRNAs may be beneficial or harmful to cell
 CC survival. If a particular microRNA is known to be beneficial, an
 CC appropriate isolated microRNA of the invention may be introduced into a
 CC cell to promote survival. Conversely, if a particular microRNA is known
 CC to be harmful (e.g., one known to induce apoptosis or induce cancer),
 CC then an appropriate anti-microRNA of the invention can be introduced into
 CC a cell to inhibit microRNA activity. Additionally, the anti-microRNAs or
 CC microRNAs of the invention may be introduced into a cell to study the
 CC function of the microRNA. Sequences AEB79321-AEB79426 represent
 CC specifically claimed Caenorhabditis elegans microRNAs upon which
 CC microRNAs of the invention may be based and which are targets for anti-
 CC microRNAs of the invention.

XX SQ Sequence 22 BP; 5 A; 5 C; 5 G; 0 T; 7 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 14; Length 22;
 Best Local Similarity 83.3%; Pred. No. 4.6e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CATCAAGGTGGCCGAGA 18
 ||||| :||| :|||
 Db 20 CATCAAGCTGGCTGTA 3

RESULT 13

AEB79630

ID AEB79630 standard; RNA; 22 BP.

XX AEB79630;

XX 20-OCT-2005 (first entry)

XX Caenorhabditis elegans Cel-miR-2-targeted anti-microRNA, SEQ:454.

XX RNA interference; gene silencing; anti-microRNA; anti-miRNA;
 XX microRNA inhibitor; miRNA inhibitor; gene expression; gene regulation;
 XX ss.

XX Caenorhabditis elegans.

XX US2005182005-A1.

XX 18-AUG-2005.

XX 13-MAY-2004; 2004US-00845057.

XX 13-FEB-2004; 2004US-00778908.

XX (TUSC/) TUSCHL T H.
 XX (LAND/) LANDTHALER M.
 XX (WEIS/) MEISTER G.
 XX (PFEF/) PFEFFER S.

XX Tuschl TH, Landthaler M, Meister G, Pfeiffer S;

XX WPI; 2005-554283/56.

XX New isolated single stranded anti-microRNA molecule comprising a minimum
 XX of ten moieties and a maximum of fifty moieties on a molecular backbone,
 XX useful for inhibiting micro ribonucleoprotein particle (microRNP)
 XX activity in a cell.

XX Claim 1; SEQ ID NO 454; 115pp; English.

XX The invention relates to isolated single-stranded anti-microRNA molecules
 CC capable of inhibiting microRNP (microribonucleoprotein) activity. The
 CC anti-microRNAs are: a) 10-50 bases in length; b) comprise unmodified or
 CC modified ribonucleotides; c) comprise a region of at least 10 contiguous
 CC bases identical to a portion of one of the human, mouse, rat, Drosophila
 CC or Caenorhabditis elegans anti-microRNAs shown in AEB79483-AEB79788,
 CC except that up to 30% of the bases are wobble bases, up to 10% of the
 CC contiguous bases may be insertions, deletions, mismatches or combinations
 CC thereof, and no more than 50% of these contiguous bases have
 CC deoxyribonucleotide backbones; and d) have a mismatch with the base at
 CC position 11 of the target microRNA. The invention also relates to a
 CC method of inhibiting microRNP activity in a cell using the anti-microRNAs
 CC of the invention, especially a human, mouse, rat, Drosophila or
 CC Caenorhabditis elegans anti-microRNA. The invention further relates to
 CC isolated microRNA molecules modified for increased nucleic acid resistance
 CC which are: i) 10-50 bases in length; and ii) comprise at least 10
 CC contiguous bases identical to one of the human, mouse, rat, Drosophila or
 CC Caenorhabditis elegans microRNAs shown in AEB79177-AEB79314 and AEB79321-
 CC AEB79482, except that up to 30% of the bases are wobble bases, up to 10%
 CC of the contiguous bases may be insertions, deletions, mismatches or
 CC combinations thereof, and no more than 50% of these contiguous bases have
 CC deoxyribonucleotide backbones. Preferably, these microRNAs comprise an
 CC inserted or deleted base or a base substitution at position 11. The anti-
 CC microRNAs and microRNAs of the invention are useful for modulating gene
 CC expression. As a component of animal microRNPs, microRNAs guide RNA
 CC degradation in a similar way to short interfering RNA (siRNA)-induced
 CC silencing complexes. Such microRNAs may be beneficial or harmful to cell
 CC survival. If a particular microRNA is known to be beneficial, an
 CC appropriate isolated microRNA of the invention may be introduced into a
 CC cell to promote survival. Conversely, if a particular microRNA is known
 CC to be harmful (e.g., one known to induce apoptosis or induce cancer),
 CC then an appropriate anti-microRNA of the invention can be introduced into
 CC a cell to inhibit microRNA activity. Additionally, the anti-microRNAs or
 CC microRNAs of the invention may be introduced into a cell to study the
 CC function of the microRNA. Sequences AEB79627-AEB79732 represent
 CC specifically claimed Caenorhabditis elegans microRNA-directed anti-
 CC microRNAs upon which anti-microRNAs of the invention may be based.

XX SQ Sequence 22 BP; 7 A; 5 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 14; Length 22;
 Best Local Similarity 72.2%; Pred. No. 4.6e+03;
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAGA 18
 ||:||||| :||| :|||
 Db 3 CAUCAAGCTGGCUGUGA 20

RESULT 14

ADA00062/c

ID ADA00062 standard; RNA; 23 BP.

XX ADA00062;

XX 06-NOV-2003 (first entry)

XX D. melanogaster miRNA sequence mir-2a SEQ ID NO:59.

XX Drosophila melanogaster; human; mouse; microRNA; miRNA; cytostatic;
 XX gene therapy; diagnostic; therapeutic; developmental modulator;
 XX pathogenic modulator; cancer; B-cell chronic leukaemia;
 XX tissue reprogramming; ss.

XX Drosophila melanogaster.

XX WO2003029459-A2.

XX 10-APR-2003.

XX 27-SEP-2002; 2002WO-EP010881.

PA (BITS-) BITS CO LTD.
 XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PI Barrero Roberto Antonio, Tamura T, Imanishi T, Gojobori T;
 XX Taira K, Kawasaki H;
 DR WPI; 2005-196094/20.
 XX
 PT Identifying a gene under regulation of functional RNA, involves setting
 PT ambiguity of different standards in conserved and unconserved region of
 PT functional RNA, searching for gene which is complementary to functional
 PT RNA.
 XX
 XX Example 1; Fig 5; 38pp; Japanese.
 XX
 CC The invention relates to a novel method for identifying or presuming a
 CC functional miRNA (micro RNA) molecule of base length of 16-25 and a gene
 CC which is regulated as a result of targeting by the miRNA. The method
 CC comprises determining and classifying the base sequences of functional
 CC RNA molecules into conserved and unconserved regions, setting ambiguities
 CC of different standards in these regions and searching for a candidate
 CC gene which has a base sequence complementary to the functional RNA
 CC molecule. The method of the invention may be useful for identifying a
 CC gene whose expression is under regulation by a functional RNA molecule of
 CC base length of 16-25. The method is thus useful for developing treatments
 CC for a disease or for treating a disease by controlling the biological
 CC function of the target gene. The current sequence is that of a micro RNA
 CC (miRNA)/human gene-related DNA of the invention. Specifically, human E2F
 CC transcription factor 3 (E2F3), eukaryotic translation initiation factor
 CC SA2 (EIF5A2) and forkhead box A1 (FOXA1), hepatocyte nuclear factor 3
 CC alpha, HNF3alpha) are referred to in claim 9.
 XX
 SQ Sequence 23 BP; 6 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
 Query Match 73.3%; Score 13.2; DB 14; Length 23;
 Best Local Similarity 83.3%; Pred. No. 4.6e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CATCAAGTGGCGGAGA 18
 Db 20 CATCAAGTGGCTGTGA 3
 RESULT 19
 ADF16111
 ID ADF16111 standard; DNA; 42 BP.
 AC ADF16111;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human albumin fusion protein-related PCR primer SeqID1198.
 XX
 KW albumin fusion protein; albumin activity; human serum albumin;
 KW serum osmotic pressure; shelf-life; stability; antidiabetic;
 KW gene therapy; diabetes mellitus; human; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003060071-A2.
 XX
 PD 24-JUL-2003.
 XX
 XX 23-DEC-2002; 2002WO-US040891.
 XX
 PR 21-DEC-2001; 2001US-0341811P.
 PR 24-JAN-2002; 2002US-0350358P.
 PR 28-JAN-2002; 2002US-0351360P.
 PR 26-FEB-2002; 2002US-0359370P.
 PR 28-FEB-2002; 2002US-0360000P.
 PR 27-MAR-2002; 2002US-0367500P.
 PR 08-APR-2002; 2002US-0370227P.
 PR 10-MAY-2002; 2002US-0378950P.

PR 24-MAY-2002; 2002US-0382617P.
 PR 28-MAY-2002; 2002US-0383123P.
 PR 05-JUN-2002; 2002US-0385708P.
 PR 10-JUL-2002; 2002US-0394625P.
 PR 24-JUL-2002; 2002US-0398008P.
 PR 09-AUG-2002; 2002US-0402131P.
 PR 13-AUG-2002; 2002US-0402708P.
 PR 18-SEP-2002; 2002US-0411355P.
 PR 18-SEP-2002; 2002US-0411426P.
 PR 02-OCT-2002; 2002US-0414984P.
 PR 11-OCT-2002; 2002US-0417611P.
 PR 23-OCT-2002; 2002US-0420246P.
 PR 05-NOV-2002; 2002US-0423623P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (DELZ) DELTA BIOTECHNOLOGY LTD.
 PA (PRIN-) PRINCIPIA PHARM CORP.
 XX
 PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
 XX WPI; 2003-598517/56.
 XX
 PT New albumin fusion protein, useful for preparing a composition for
 PT treating diabetes mellitus.
 XX
 PS Example 4; SEQ ID NO 1198; 24pp; English.
 XX
 CC This invention relates to a novel albumin fusion protein having albumin
 CC or biological activity. Human serum albumin is responsible for a
 CC significant proportion of the osmotic pressure of serum and also
 CC functions as a carrier of endogenous and exogenous ligands. The fusion of
 CC albumin to a therapeutic protein may increase shelf-life and stability of
 CC the therapeutic protein. The albumin fusion protein of the invention may
 CC allow production of compositions with antidiabetic activity whilst the
 CC nucleotide sequence which encodes it may be useful for gene therapy. The
 CC albumin fusion protein is useful for preparing a composition for treating
 CC diabetes mellitus. The present sequence is that of a PCR primer which may
 CC be used for amplification of a DNA sequence encoding a therapeutic
 CC protein which was fused with human albumin to create a novel albumin
 CC fusion protein of the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/publishedpct_sequences
 XX
 SQ Sequence 42 BP; 8 A; 13 C; 17 G; 4 T; 0 U; 0 Other;
 Query Match 73.3%; Score 13.2; DB 10; Length 42;
 Best Local Similarity 83.3%; Pred. No. 4.9e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CATCAAGTGGCGGAGA 18
 Db 13 CCTCAAGTGGCGGTAGA 30
 RESULT 20
 AAL32362
 ID AAL32362 standard; DNA; 51 BP.
 XX
 AC AAL32362;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human SNP oligonucleotide #5570.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiopeptin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinase; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.

XX WPI; 2003-636699/60.

XX Novel Sim-2 biomolecule transduction motif peptide or its active

PT fragment, useful for transducing a biologically active, functional and/or

PT regulatory molecule e.g., DNA, RNA into prokaryotic or eukaryotic cells.

XX

PS Disclosure; Page 91; 94pp; English.

XX

XX The present invention describes a biomolecule transduction motif

CC designated SIM-2-BTM. The SIM-2-BTM peptide has a potential to transduce

CC many biological response modifiers effectively into the cytoplasm,

CC intracellular organelles or nucleus of prokaryotic or eukaryotic cells in

CC vivo and in vitro, and the related technological methods for using SIM-2-

CC BTM. SIM-2-BTM can be used in drug delivery systems, for the development

CC of recombinant protein vaccines or DNA/RNA vaccines, in gene and protein

CC therapy, in the production of pharmacologically or medically useful

CC protein, or in pharmaceutical drug therapy. The present sequence

CC represents a primer which is used in the exemplification of the present

CC invention.

XX

SQ Sequence 72 BP; 18 A; 16 C; 18 G; 20 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 9; Length 72;

Best Local Similarity 83.3%; Pred. No. 5.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCGGAGA 18

||||| ||||| ||

Db 49 CATCAATGGCGCGCGGA 32

RESULT 23

ACF04460/c

ID ACF04460 standard; DNA; 72 BP.

XX ACF04460;

DT 04-DEC-2003 (first entry)

XX Biomolecule transduction motif Mph-1 vector pCDNA3-ZAL12 primer #4.

XX

KW Transduction motif; MPH-1-BTM; Mph-1; drug delivery system;

KW protein vaccine; nucleic acid vaccine; gene therapy; protein therapy;

KW virucide; antibacterial; fungicide; cytostatic; antidiabetic;

KW immunosuppressive; PCR; primer; ss.

XX

OS Unidentified.

XX

XX WO2003059941-A1.

XX

XX 24-JUL-2003.

XX

XX 20-JAN-2003; 2003WO-KR000122.

XX

XX 19-JAN-2002; 2002KR-00003183.

XX

XX (LEES/) LEE S.

XX

XX Lee S, Lee S, Suh B, Chae W, Kim J, Lee J;

PI

XX WPI; 2003-598502/56.

XX

XX New biomolecule transduction motif Mph-1 peptide, useful for transducing

PT a biologically active, functional and/or regulatory molecule into

PT prokaryotic or eukaryotic cells, for drug delivery system, or gene and

PT protein therapy.

XX

PS Disclosure; Page 91; 93pp; English.

XX

XX The present invention relates to a biomolecule transduction motif Mph-1

CC peptide or its active fragment, which can be used for transducing a

CC biologically active, functional and/or regulatory molecule into

CC prokaryotic or eukaryotic cells. The biomolecule transduction motif Mph-1

CC peptide, its fusion protein, expression vector and biomolecule

CC transduction complex are useful for transducing a biologically active,

CC functional and/or regulatory molecule into prokaryotic or eukaryotic

CC cells. The Mph-1 peptide is also useful for drug delivery systems,

CC developing new recombinant protein or DNA/RNA vaccines against viruses,

CC bacteria, mold or various cancer cells, gene and protein therapy,

CC producing pharmacologically or medicinally useful proteins, or pharmaco-

CC medicinal drug therapy. In particular, the biomolecule transduction motif

CC Mph-1 peptide is useful for producing protein drugs with natural folding

CC structure and function e.g. Mph1-insulin fusion protein for treating

CC diabetes. The present sequence is a PCR primer used to amplify a vector

CC containing the coding sequence for the peptide of the invention

XX

SQ Sequence 72 BP; 18 A; 16 C; 18 G; 20 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 9; Length 72;

Best Local Similarity 83.3%; Pred. No. 5.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCGGAGA 18

||||| ||||| ||

Db 49 CATCAATGGCGCGCGGA 32

RESULT 24

ADR83553/c

ID ADR83553 standard; DNA; 76 BP.

XX ADR83553;

AC ADR83553;

XX

DT 02-DEC-2004 (first entry)

XX

XX Human DNA related to regulating mammalian cells using miRNAs Seq 455.

XX

KW human; ds; miRNA; microRNA; ontogenesis; cell therapy; cancer;

KW immune disease; nerve disorder; amyotrophic lateral sclerosis;

KW Parkinson's disease; Alzheimer's disease; inflammatory disease;

KW siRNA silencing precursor; cytostatic; immunosuppressive; neurotropic;

KW neuroprotective; antiinflammatory; immunotherapy.

XX

OS Homo sapiens.

XX

XX WO2004076622-A2.

XX

XX 10-SEP-2004.

XX

XX 10-FEB-2004; 2004WO-JP001433.

XX

XX 10-FEB-2003; 2003US-0445829P.

XX

XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX

XX Taira K, Kawasaki H;

PI

XX WPI; 2004-653393/63.

XX

XX Modulating expression of a target gene in a cell, for treating cancer, an

PT immune disease, or a nerve disorder, comprises introducing into the cell

PT a polynucleotide that forms a duplex region with an mRNA transcribed from

PT the target gene.

XX

XX Disclosure; SEQ ID NO 455; 865pp; English.

XX

XX This invention relates to a novel method for modulating the expression of

CC a target gene in a cell. Specifically, it refers to the introduction into

CC a cell of a polynucleotide that forms a duplex region with an mRNA

CC transcribed from the target gene, where the duplex region comprises a

CC mammalian miRNA target region i.e. a non-coding microRNA (miRNA) that

CC regulates mRNA at a post-transcriptional level. The present invention

CC describes a method for controlling ontogenesis of a mammal, function of a

CC mammalian cell, differentiation of a mammalian cell or viability of a

CC mammalian cell in the post-transcriptional phase, which comprises

CC introducing a plasmid vector comprising a promoter and nucleic acid
CC molecule expressing an miRNA or siRNA silencing precursor to the miRNA.
CC Accordingly, it provides a cell therapy method for treating cancer,
CC immune disease, nerve disorder (e.g. amyotrophic lateral sclerosis,
CC Parkinson's disease, or Alzheimer's disease) or an inflammatory disease
CC by introducing into the cell the miRNA, siRNA silencing precursor to the
CC miRNA or the plasmid vector. As such, they can be developed into
CC pharmaceutical compositions that exhibit cytostatic, immunosuppressive,
CC neurotropic, neuroprotective and antiinflammatory activities and hence can
CC be used for immunotherapy. This polynucleotide sequence is a human DNA
CC sequence related to the regulation of mammalian cells using miRNAs to
CC modulate expression, given in an exemplification of the invention. NOTE:
CC This sequence is given in the sequence listing but is not further
CC referred to in the specification.

XX SQ Sequence 76 BP; 15 A; 18 C; 21 G; 22 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 13; Length 76;
Best Local Similarity 83.3%; Pred. No. 5.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAGA 18
Db 68 CATCAAGCTGGCTGTGA 51
|||||

RESULT 25

AAQ27315
ID AAQ27315 standard; DNA; 18 BP.

XX AC AAQ27315;

XX DT 23-SEP-2004 (revised)

XX DT 25-MAR-2003 (revised)

XX DT 01-FEB-1993 (first entry)

XX DE PCR primer Cbtaext for TCR Beta-Chain genes.

XX KW TCR, beta chain; rheumatoid arthritis; multiple sclerosis;
XX KW autoimmune disease; diabetes; T-cell lymphoma; vaccination; immunisation;
XX KW experimental allergic encephalomyelitis; ss.

XX OS Synthetic.

XX PN WO9212996-A2.

XX PD 06-AUG-1992.

XX PF 21-JAN-1992; 92WO-US000482.

XX PR 22-JAN-1991; 91US-00644611.

XX PA (IMMU-) IMMUNE RESPONSE CORP.

XX PI Howell MD, Brostoff SW, Carlo DJ;

XX DR WPI; 1992-284600/34.

XX PT Treatment of auto:immune diseases e.g. rheumatoid arthritis - using
XX PT vaccine contg. T-cell receptors from surface of T-cells which mediate the
XX PT diseases.

XX PS Example 10; Page 48; 87pp; English.

XX CC This sequence represents a PCR primer used to amplify the T cell receptor
XX CC beta chain genes in a two stage amplification reaction with nested pairs
XX CC of primers. See also AAQ27310-7. (Updated on 25-MAR-2003 to correct PN
XX CC field.)

XX CC Revised record issued on 23-SEP-2004 : Correction to keywords

XX SQ Sequence 18 BP; 5 A; 5 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 72.2%; Score 13; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AAGGTGGCCGAGA 18
|||||

Db 5 AAGGTGGCCGAGA 17
|||||

Search completed: March 3, 2006, 08:00:20
Job time : 124.534 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:29:32 ; Search time 23.6441 Seconds
 (without alignments)
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Title: US-10-655-801-19
 Perfect score: 18
 Sequence: 1 catcaaggtgcccagaga 18

Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1395746

Minimum DB seq length: 0
 Maximum DB seq length: 80

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

Database : Issued Patents NA.*
 1: /cgn2_6/prodata/1/ina/1 COMB.seq.*
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 7: /cgn2_6/prodata/1/ina/PP COMB.seq.*
 8: /cgn2_6/prodata/1/ina/RE COMB.seq.*
 9: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14	77.8	25	3	US-09-396-196G-7331
C 2	14	77.8	25	3	US-09-396-196G-7332
C 3	14	77.8	25	3	US-09-396-196G-28185
C 4	13	72.2	18	2	US-08-466-860-53
C 5	13	72.2	18	3	US-08-472-040A-53
C 6	13	72.2	18	3	US-08-276-776-53
C 7	13	72.2	18	3	US-08-471-209-53
C 8	12.8	71.1	20	3	US-09-593-711A-216
C 9	12.8	71.1	25	3	US-09-396-196G-101443
C 10	12.8	71.1	26	3	US-08-943-731-282
C 11	12.8	71.1	52	2	US-08-629-039-5
C 12	12.4	68.9	19	3	US-09-696-791-874
C 13	12.4	68.9	24	3	US-09-518-914-24
C 14	12.4	68.9	25	3	US-09-396-196G-14358
C 15	12.4	68.9	25	3	US-09-396-196G-14359
C 16	12.4	68.9	27	2	US-08-808-793-31
C 17	12.4	68.9	45	3	US-09-518-914-18
C 18	12.4	68.9	50	3	US-10-131-827-4058
C 19	12.2	67.8	20	3	US-08-864-357F-19
C 20	12.2	67.8	22	3	US-09-954-736A-7
C 21	12.2	67.8	22	3	US-09-872-051-14
C 22	12.2	67.8	23	3	US-10-402-839A-2
C 23	12.2	67.8	23	3	US-10-402-839A-4
C 24	12.2	67.8	23	3	US-10-402-839A-8

Sequence 118719,	25	3	US-09-396-196G-118719	67.8	12.2	C 25
Sequence 118720,	25	3	US-09-396-196G-118720	67.8	12.2	C 26
Sequence 173, Appl	30	3	US-08-711-417C-173	67.8	12.2	C 27
Sequence 14, Appl	30	3	US-08-733-622C-14	67.8	12.2	C 28
Sequence 173, Appl	30	3	US-09-723-909-173	67.8	12.2	C 29
Sequence 14, Appl	30	3	US-09-019-348-14	67.8	12.2	C 30
Sequence 1745, A	17	3	US-09-396-196G-31745	66.7	12	C 31
Sequence 10250, A	17	3	US-09-866-108A-10250	65.6	11.8	C 32
Sequence 10251, A	17	3	US-09-866-108A-10251	65.6	11.8	C 33
Sequence 10252, A	17	3	US-09-866-108A-10252	65.6	11.8	C 34
Sequence 353, Appl	17	3	US-09-404-912-353	65.6	11.8	C 35
Sequence 11, Appl	18	3	US-09-593-711A-11	65.6	11.8	C 36
Sequence 156, Appl	20	3	US-09-488-671-156	65.6	11.8	C 37
Sequence 43, Appl	21	3	US-09-865-993-43	65.6	11.8	C 38
Sequence 26, Appl	21	3	US-09-896-915-26	65.6	11.8	C 39
Sequence 3, Appl	22	3	US-09-068-880-3	65.6	11.8	C 40
Sequence 1, Appl	24	3	US-09-011-600-1	65.6	11.8	C 41
Sequence 1, Appl	24	3	US-09-722-348-1	65.6	11.8	C 42
Sequence 12, Appl	24	3	US-09-600-031-12	65.6	11.8	C 43
Sequence 15142, A	25	3	US-09-866-108A-15142	65.6	11.8	C 44
Sequence 15143, A	25	3	US-09-866-108A-15143	65.6	11.8	C 45
Sequence 15144, A	25	3	US-09-866-108A-15144	65.6	11.8	C 46
Sequence 15145, A	25	3	US-09-866-108A-15145	65.6	11.8	C 47
Sequence 15146, A	25	3	US-09-866-108A-15146	65.6	11.8	C 48
Sequence 15147, A	25	3	US-09-866-108A-15147	65.6	11.8	C 49
Sequence 15148, A	25	3	US-09-866-108A-15148	65.6	11.8	C 50
Sequence 15149, A	25	3	US-09-866-108A-15149	65.6	11.8	C 51
Sequence 15150, A	25	3	US-09-866-108A-15150	65.6	11.8	C 52
Sequence 15151, A	25	3	US-09-866-108A-15151	65.6	11.8	C 53
Sequence 15152, A	25	3	US-09-866-108A-15152	65.6	11.8	C 54
Sequence 66324, A	25	3	US-09-396-196G-66324	65.6	11.8	C 55
Sequence 105959,	25	3	US-09-396-196G-105959	65.6	11.8	C 56
Sequence 1, Appl	29	3	US-08-440-566-1	65.6	11.8	C 57
Sequence 27, Appl	29	3	US-09-896-915-27	65.6	11.8	C 58
Sequence 3, Appl	30	2	US-08-321-613-3	65.6	11.8	C 59
Sequence 70, Appl	30	3	US-08-938-830-70	65.6	11.8	C 60
Sequence 70, Appl	30	3	US-09-068-377-70	65.6	11.8	C 61
Sequence 1041, Ap	38	3	US-09-474-432B-1041	65.6	11.8	C 62
Sequence 1146, Ap	38	3	US-09-474-432B-1146	65.6	11.8	C 63
Sequence 1040, Ap	38	3	US-09-476-387-1040	65.6	11.8	C 64
Sequence 1145, Ap	38	3	US-09-476-387-1145	65.6	11.8	C 65
Sequence 3189, Ap	47	3	US-09-422-978-3189	65.6	11.8	C 66
Sequence 7469, Ap	50	3	US-10-131-827-7469	65.6	11.8	C 67
Sequence 8112, Ap	50	3	US-10-131-827-8112	65.6	11.8	C 68
Sequence 21, Appl	52	2	US-08-358-918-21	65.6	11.8	C 69
Sequence 21, Appl	52	2	US-08-883-795A-21	65.6	11.8	C 70
Sequence 41, Appl	55	3	US-09-386-642-41	65.6	11.8	C 71
Sequence 43, Appl	55	3	US-09-386-642-42	65.6	11.8	C 72
Sequence 43, Appl	55	3	US-09-386-642-43	65.6	11.8	C 73
Sequence 44, Appl	56	3	US-09-386-642-44	65.6	11.8	C 74
Sequence 5, Appl	56	2	US-08-883-795A-5	65.6	11.8	C 75
Sequence 18, Appl	70	3	US-09-364-380-18	65.6	11.8	C 76
Sequence 34, Appl	73	2	US-08-434-001-34	65.6	11.8	C 77
Sequence 34, Appl	73	2	US-08-433-585-34	65.6	11.8	C 78
Sequence 34, Appl	73	2	US-08-434-425-34	65.6	11.8	C 79
Sequence 34, Appl	73	2	US-08-437-667-34	65.6	11.8	C 80
Sequence 34, Appl	73	3	US-08-906-955-34	65.6	11.8	C 81
Sequence 34, Appl	73	3	US-08-945-909-34	65.6	11.8	C 82
Sequence 34, Appl	73	3	US-09-396-002A-34	65.6	11.8	C 83
Sequence 34, Appl	73	3	US-10-077-319-34	65.6	11.8	C 84
Sequence 34, Appl	73	6	PCT-US96-06060-34	65.6	11.8	C 85
Sequence 26523, A	74	3	US-09-270-767-26523	65.6	11.8	C 86
Sequence 426, App	19	3	US-09-338-907-426	64.4	11.6	C 87
Sequence 426, App	19	3	US-09-218-207-426	64.4	11.6	C 88
Sequence 23, Appl	20	2	US-08-887-365-23	64.4	11.6	C 89
Sequence 12, Appl	20	3	US-08-914-961-12	64.4	11.6	C 90
Sequence 27, Appl	20	3	US-09-357-073-27	64.4	11.6	C 91
Sequence 16, Appl	20	3	US-09-489-765A-16	64.4	11.6	C 92
Sequence 11, Appl	21	3	US-08-913-547-11	64.4	11.6	C 93
Sequence 1746, Ap	21	3	US-09-657-472-1746	64.4	11.6	C 94
Sequence 6, Appl	23	3	US-10-402-839A-6	64.4	11.6	C 95
Sequence 10, Appl	23	3	US-10-402-839A-10	64.4	11.6	C 96
						C 97

c 98 11.6 64.4 23 3 US-10-402-839A-12 Sequence 12, Appl
c 99 11.6 64.4 23 3 US-10-402-839A-15 Sequence 15, Appl
c 100 11.6 64.4 23 3 US-10-402-839A-21 Sequence 21, Appl

ALIGNMENTS

RESULT 1

US-09-396-196G-7331/c
; Sequence 7331, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7331
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-7331

Query Match 77.8%; Score 14; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCC 14
| | | | | | | | | |
Db 23 CATCAAGGTGGCC 10

RESULT 2

US-09-396-196G-7332/c
; Sequence 7332, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7332
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-7332

Query Match 77.8%; Score 14; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCC 14
| | | | | | | | | |
Db 17 CATCAAGGTGGCC 4

RESULT 3

US-09-396-196G-28185
; Sequence 28185, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28185
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-28185

Query Match 77.8%; Score 14; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AAAGTGGCGGAGA 18
| | | | | | | | | |
Db 8 AAAGTGGCGGAGA 21

RESULT 4

US-08-466-860-53
; Sequence 53, Application US/08466860
; Patent No. 5985552
; GENERAL INFORMATION:
; APPLICANT: HOWELL, MARK D.
; APPLICANT: BROSTOFF, STEVEN W.
; APPLICANT: CARLO, DENNIS J.
; TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
; TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,860
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,867
; FILING DATE: 24-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 9107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-466-860-53

Query Match 72.2% Score 13; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AAGGTGGCCGAGA 18
Db 5 AAGGTGGCCGAGA 17

RESULT 5
US-08-472-040A-53
Sequence 53, Application US/08472040A
Patent No. 6090387
GENERAL INFORMATION:
APPLICANT: HOWELL, MARK D.
APPLICANT: BROSTOFF, STEVEN W.
TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
TITLE OF INVENTION: POPULATIONS
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,040A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 1641
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-472-040A-53

Query Match 72.2% Score 13; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AAGGTGGCCGAGA 18
Db 5 AAGGTGGCCGAGA 17

RESULT 6
US-08-276-776-53
Sequence 53, Application US/08276776
Patent No. 6207645
GENERAL INFORMATION:
APPLICANT: HOWELL, MARK D.

APPLICANT: BROSTOFF, STEVEN W.
APPLICANT: CARLO, DENNIS J.
TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
TITLE OF INVENTION: POPULATIONS
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,776
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/813,867
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 9107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-276-776-53

Query Match 72.2% Score 13; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AAGGTGGCCGAGA 18
Db 5 AAGGTGGCCGAGA 17

RESULT 7
US-08-471-209-53
Sequence 53, Application US/08471209
Patent No. 6221352
GENERAL INFORMATION:
APPLICANT: HOWELL, MARK D.
APPLICANT: BROSTOFF, STEVEN W.
TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
TITLE OF INVENTION: POPULATIONS
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,040A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 1641
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-472-040A-53

Query Match 72.2% Score 13; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AAGGTGGCCGAGA 18
Db 5 AAGGTGGCCGAGA 17

RESULT 6
US-08-276-776-53
Sequence 53, Application US/08276776
Patent No. 6207645
GENERAL INFORMATION:
APPLICANT: HOWELL, MARK D.

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA: US/08/471,209
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION NUMBER: US 07/813,867
;; FILING DATE: 24-DEC-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CAMPBELL, KATHRYN
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-IM 9107
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-535-9001
;; TELEFAX: 619-535-8949
;; INFORMATION FOR SEQ ID NO: 53:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-471-209-53

Query Match 72.2%; Score 13; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AAGTGGCCGAGA 18
| | | | | | | | | |
Db 5 AAGTGGCCGAGA 17

RESULT 8

US-09-593-711A-216/c
;; Sequence 216, Application US/09593711A
;; Patent No. 6271030
;; GENERAL INFORMATION:
;; APPLICANT: Brett P. Monia
;; APPLICANT: Madeline M. Butler
;; APPLICANT: Jacqueline Wyatt
;; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
;; FILE REFERENCE: RTS-0118
;; CURRENT APPLICATION NUMBER: US/09/593,711A
;; CURRENT FILING DATE: 2000-06-14
;; NUMBER OF SEQ ID NOS: 244
;; SEQ ID NO 216
;; LENGTH: 20
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Antisense Oligonucleotide
;; US-09-593-711A-216

Query Match 71.1%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATCAAAGTGGCCGAG 17
| | | | | | | | | |
Db 17 ATCAAAGTGGCTGAG 2

RESULT 9

US-09-396-196G-101443
;; Sequence 101443, Application US/09396196G
;; Patent No. 6821724
;; GENERAL INFORMATION:
;; APPLICANT: Michael Mittmann
;; APPLICANT: David Mack
;; APPLICANT: David Lockhart
;; APPLICANT: Affymetrix, Inc.
;; TITLE OF INVENTION: Methods of Genetic Analysis

;; FILE REFERENCE: 3101.1
;; CURRENT APPLICATION NUMBER: US/09/396,196G
;; CURRENT FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: 60/100,678
;; PRIOR FILING DATE: 1998-09-17
;; NUMBER OF SEQ ID NOS: 127806
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 101443
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: mus musculus
;; US-09-396-196G-101443

Query Match 71.1%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATCAAAGTGGCCGAG 17
| | | | | | | | | |
Db 10 ATCAAAGTGGCTGAG 25

RESULT 10

US-08-943-731-282
;; Sequence 282, Application US/08943731
;; Patent No. 6265157
;; GENERAL INFORMATION:
;; APPLICANT: PROCKOP, DARWIN J.
;; APPLICANT: SPOTILA, LORETTA D.
;; APPLICANT: DELTAS, CONSTANTINOS D.
;; APPLICANT: SEREDA, LARISA
;; APPLICANT: LARSON, ANDREA W.
;; APPLICANT: PACK, MICHAEL
;; APPLICANT: COLIGE, ALAIN
;; APPLICANT: EARLY, JAMES
;; APPLICANT: KORKKO, JARMO
;; APPLICANT: ALA-KOKKO, LEENA, et al.
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
;; TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
;; NUMBER OF SEQUENCES: 666
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
;; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
;; STREET: FLR
;; CITY: PHILADELPHIA
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103-7086
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/943,731
;; FILING DATE: 03-OCT-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/212,322
;; FILING DATE: 14-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/803,628
;; FILING DATE: 03-DEC-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DOYLE LEARY Ph.D., KATHRYN
;; REGISTRATION NUMBER: 36,317
;; REFERENCE/DOCKET NUMBER: 9598-27
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-965-1284
;; TELEFAX: 215-567-2991
;; TELEX: 831-494
;; INFORMATION FOR SEQ ID NO: 282:
;; SEQUENCE CHARACTERISTICS:

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; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-943-731-282

Query Match      71.1%; Score 12.8; DB 3; Length 26;
Best Local Similarity 87.5%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCAAAGTGGCCGAG 18
Db 4 TCAAGAGGCGAG 19

RESULT 11
US-08-629-039-5/c
; Sequence 5, Application US/08629039
; Patent No. 5958736
; GENERAL INFORMATION:
; APPLICANT: STAHL, Stefan
; APPLICANT: NYGREN, Per-Ake
; APPLICANT: HANSSON, Marianne
; APPLICANT: UHLEN, Mathias
; APPLICANT: NGUYEN, Thien N
; TITLE OF INVENTION: RECOMBINANT DNA CODING FOR SIGNAL
; TITLE OF INVENTION: PEPTIDE, SELECTIVE INTERACTING POLYPEPTIDE AND MEMBRANE
; TITLE OF INVENTION: ANCHORING SEQUENCE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/629,039
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/140,138
; FILING DATE: 03-NOV-1993
; APPLICATION NUMBER: SE 9101433-2
; FILING DATE: 13-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 003300-295
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; MOLECULE TYPE: linear
; MOLECULE TYPE: DNA (genomic)
US-08-629-039-5

Query Match      71.1%; Score 12.8; DB 2; Length 52;
Best Local Similarity 87.5%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATCAAAGTGGCCGAG 17
Db 1 ATCAAAGTGGCCGAG 17

; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-696-791-874

Query Match      68.9%; Score 12.4; DB 3; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGTGGCCGAG 17
Db 4 CAAAGTGGCCGAG 17

RESULT 12
US-09-696-791-874
; Sequence 874, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 874
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdk8 ribozyme binding site
US-09-696-791-874

Query Match      68.9%; Score 12.4; DB 3; Length 19;
Best Local Similarity 92.9%; Pred. No. 2.7e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGTGGCCGAG 17
Db 4 CAAAGTGGCCGAG 17

RESULT 13
US-09-518-914-24
; Sequence 24, Application US/09518914
; Patent No. 6413731
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Ogozalek, Kristine L.
; APPLICANT: Lakhiani, Parul P.
; APPLICANT: Adham, Nika
; TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS
; FILE REFERENCE: 59138-A/JPW
; CURRENT APPLICATION NUMBER: US/09/518,914
; CURRENT FILING DATE: 2000-03-03
; EARLIER APPLICATION NUMBER: US 09/303,593
; EARLIER FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-09-518-914-24

Query Match      68.9%; Score 12.4; DB 3; Length 24;
Best Local Similarity 92.9%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATCAAGTGGCC 14
Db 11 CACCAAGTGGCC 24

RESULT 14
US-09-396-196G-14358/c
; Sequence 14358, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
```

```
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14358
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-14358

Query Match      68.9%; Score 12.4; DB 3; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  5  AAAGTGGCCGAGA 18
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Db   25 AACGGTGGCCGAGA 12

RESULT 15
US-09-396-196G-14359/c
; Sequence 14359, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14359
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-14359

Query Match      68.9%; Score 12.4; DB 3; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  5  AAAGTGGCCGAGA 18
    |||||
Db   22 AACGGTGGCCGAGA 9

RESULT 16
US-08-808-793-31/c
; Sequence 31, Application US/08808793
; Patent No. 5858713
; GENERAL INFORMATION:
; APPLICANT: Soderlund, David M.
; APPLICANT: Ingles, Patricia J.
; TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
; TITLE OF INVENTION: AND USE THEREOF
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester

Query Match      68.9%; Score 12.4; DB 3; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  5  AAAGTGGCCGAGA 18
    |||||
Db   22 AACGGTGGCCGAGA 9

RESULT 17
US-09-518-914-18/c
; Sequence 18, Application US/09518914
; Patent No. 6413731
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Ogozalek, Kristine L.
; APPLICANT: Lakhiani, Parul P.
; APPLICANT: Adham, Nika
; TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS
; FILE REFERENCE: 59138-A/JPW
; CURRENT APPLICATION NUMBER: US/09/518,914
; CURRENT FILING DATE: 2000-03-03
; EARLIER APPLICATION NUMBER: US 09/303,593
; EARLIER FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
; US-09-518-914-18

Query Match      68.9%; Score 12.4; DB 3; Length 45;
Best Local Similarity 92.9%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,793
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,361
; FILING DATE: 24-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/012,649
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-808-793-31

Query Match      68.9%; Score 12.4; DB 2; Length 27;
Best Local Similarity 92.9%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  CATCAAAGGTGGCC 14
    |||||
Db   16 CCTCAAAGGTGGCC 3

RESULT 17
US-09-518-914-18/c
; Sequence 18, Application US/09518914
; Patent No. 6413731
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Ogozalek, Kristine L.
; APPLICANT: Lakhiani, Parul P.
; APPLICANT: Adham, Nika
; TITLE OF INVENTION: DNA ENCODING SNORF36a AND SNORF36b RECEPTORS
; FILE REFERENCE: 59138-A/JPW
; CURRENT APPLICATION NUMBER: US/09/518,914
; CURRENT FILING DATE: 2000-03-03
; EARLIER APPLICATION NUMBER: US 09/303,593
; EARLIER FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
; US-09-518-914-18

Query Match      68.9%; Score 12.4; DB 3; Length 45;
Best Local Similarity 92.9%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 CATCAAGGTGGCC 14
 Db 34 CACCAAGGTGGCC 21

RESULT 18

US-10-131-827-4058
 ; Sequence 4058, Application US/10131827
 ; Patent No. 6905827
 ; GENERAL INFORMATION:
 ; APPLICANT: Wohlgemuth, Jay
 ; APPLICANT: Fry, Kirk
 ; APPLICANT: Woodward, Robert
 ; APPLICANT: Ly, Ngoc
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
 ; FILE REFERENCE: 506612000120
 ; CURRENT APPLICATION NUMBER: US/10/131,827
 ; CURRENT FILING DATE: 2002-09-06
 ; PRIOR APPLICATION NUMBER: US 10/006,290
 ; PRIOR FILING DATE: 2001-10-22
 ; PRIOR APPLICATION NUMBER: US 60/296,764
 ; PRIOR FILING DATE: 2001-06-08
 ; NUMBER OF SEQ ID NOS: 9090
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4058
 ; LENGTH: 50
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: US-10-827-4058

Query Match 68.9%; Score 12.4; DB 3; Length 50;
 Best Local Similarity 92.9%; Pred. No. 3.1e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AAAGTGGCCGAGA 18
 Db 17 AAAGTGGCCGAGA 30

RESULT 19

US-08-864-357F-19
 ; Sequence 19, Application US/08864357F
 ; Patent No. 6255281
 ; GENERAL INFORMATION:
 ; APPLICANT: Claragen, Inc. & NIH
 ; TITLE OF INVENTION: Use of Recombinant Human Uteroglobin in Treatment of Inflammato
 ; FILE REFERENCE: 116142/2
 ; CURRENT APPLICATION NUMBER: US/08/864,357F
 ; CURRENT FILING DATE: 1997-05-28
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 19
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: artificial
 ; FEATURE:
 ; OTHER INFORMATION: mGAPDH-r primer sequence
 ; US-08-864-357F-19

Query Match 67.8%; Score 12.2; DB 3; Length 20;
 Best Local Similarity 82.4%; Pred. No. 3.5e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAG 17
 Db 3 CATCGAAGTGGGAAGAG 19

RESULT 20

US-09-954-736A-7/c

; Sequence 7, Application US/09954736A
 ; Patent No. 6689744
 ; GENERAL INFORMATION:
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Koepfen, Hartmut
 ; APPLICANT: Ross, Sarajane
 ; APPLICANT: Shou, Jianyong
 ; TITLE OF INVENTION: NOTCH RECEPTOR AGONISTS AND USES
 ; FILE REFERENCE: P1848R1
 ; CURRENT APPLICATION NUMBER: US/09/954,736A
 ; CURRENT FILING DATE: 2001-09-17
 ; PRIOR APPLICATION NUMBER: US 60/234,674
 ; PRIOR FILING DATE: 2000-09-22
 ; NUMBER OF SEQ ID NOS: 21
 ; SEQ ID NO 7
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Oligonucleotide Probe
 ; US-09-954-736A-7

Query Match 67.8%; Score 12.2; DB 3; Length 20;
 Best Local Similarity 82.4%; Pred. No. 3.5e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAG 17
 Db 17 CGTCAAGGTGGGAGGAG 1

RESULT 21

US-09-872-051-14/c
 ; Sequence 14, Application US/09872051
 ; Patent No. 6825400
 ; GENERAL INFORMATION:
 ; APPLICANT: Monsanto Co
 ; APPLICANT: Behr, Carl
 ; APPLICANT: Hironaka, Catherine
 ; APPLICANT: Heck, Gregory
 ; APPLICANT: You, Jinsong
 ; TITLE OF INVENTION: Corn Event PV-ZMGT32(nk603) and Composition and Methods for Dete
 ; FILE REFERENCE: 38-21(52258)B
 ; CURRENT APPLICATION NUMBER: US/09/872,051
 ; CURRENT FILING DATE: 2001-06-01
 ; PRIOR APPLICATION NUMBER: 60/213,567
 ; PRIOR FILING DATE: 2000-06-22
 ; PRIOR APPLICATION NUMBER: 60/241,215
 ; PRIOR FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: 60/240,014
 ; PRIOR FILING DATE: 2000-10-13
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 14
 ; LENGTH: 22
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: source
 ; LOCATION: (1)..(22)
 ; OTHER INFORMATION: fully synthesized
 ; US-09-872-051-14

Query Match 67.8%; Score 12.2; DB 3; Length 22;
 Best Local Similarity 82.4%; Pred. No. 3.5e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATCAAGGTGGCCGAGA 18
 Db 22 ATAAAGGTGGCCCAAA 6

RESULT 22

US-10-402-839A-2/c
; Sequence 2, Application US/10402839A
; Patent No. 6955883
; GENERAL INFORMATION:
; APPLICANT: Perlegen Sciences
; TITLE OF INVENTION: Life Sciences Business Systems and Methods
; FILE REFERENCE: 29202-704
; CURRENT APPLICATION NUMBER: US/10/402,839A
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 10/107,508
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 23
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: exemplary allele with variants
US-10-402-839A-2

Query Match 67.8%; Score 12.2; DB 3; Length 23;
Best Local Similarity 82.4%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAG 17
| | | | | | | | | | | | | | | | | | | | |
Db 21 CGTCAAGGTGGCCAG 5

RESULT 23

US-10-402-839A-4/c
; Sequence 4, Application US/10402839A
; Patent No. 6955883
; GENERAL INFORMATION:
; APPLICANT: Perlegen Sciences
; TITLE OF INVENTION: Life Sciences Business Systems and Methods
; FILE REFERENCE: 29202-704
; CURRENT APPLICATION NUMBER: US/10/402,839A
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 10/107,508
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 23
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: exemplary allele with common variants grouped into haplotypes
US-10-402-839A-4

Query Match 67.8%; Score 12.2; DB 3; Length 23;
Best Local Similarity 82.4%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAG 17
| | | | | | | | | | | | | | | | | | | | |
Db 21 CGTCAAGGTGGCCAG 5

RESULT 24

US-10-402-839A-8/c
; Sequence 8, Application US/10402839A
; Patent No. 6955883
; GENERAL INFORMATION:
; APPLICANT: Perlegen Sciences
; TITLE OF INVENTION: Life Sciences Business Systems and Methods
; FILE REFERENCE: 29202-704
; CURRENT APPLICATION NUMBER: US/10/402,839A
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 10/107,508

; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 23
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: exemplary allele with common variants
US-10-402-839A-8

Query Match 67.8%; Score 12.2; DB 3; Length 23;
Best Local Similarity 82.4%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAG 17
| | | | | | | | | | | | | | | | | | | | |
Db 21 CGTCAAGGTGGCCAG 5

RESULT 25

US-09-396-196G-118719/c
; Sequence 118719, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118719
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-118719

Query Match 67.8%; Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATCAAGGTGGCCGAGA 18
| | | | | | | | | | | | | | | | | | | | |
Db 25 ACCAAAGGTGCCAAGA 9

Search completed: March 3, 2006, 07:34:52
Job time : 24.6441 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:34:36 ; Search time 221.11 Seconds
(without alignments)
673.188 Million cell updates/sec

Title: US-10-655-801-19
Perfect score: 18
Sequence: 1 catcaaggtgcccaga 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11282798

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications NA.Main:
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	9	US-10-182-049-19
2	14.4	80.0	25	8	US-10-719-900-244282
3	14.4	80.0	25	10	US-11-036-317-138400
4	14.4	80.0	25	10	US-11-036-317-203113
5	14.4	80.0	25	10	US-11-036-317-231362
6	14.4	80.0	25	10	US-11-036-317-270126
7	14.4	80.0	25	10	US-11-036-317-340096
8	14.4	80.0	25	10	US-11-036-317-364267
9	14.4	80.0	25	10	US-11-036-317-365442
10	14.4	80.0	25	10	US-11-036-317-366373
11	14.4	80.0	25	10	US-11-036-317-895040
12	14.4	80.0	25	10	US-11-036-317-957650
13	14.4	80.0	25	10	US-11-036-317-972134
14	14.4	80.0	25	10	US-11-036-317-972700
15	14	77.8	25	9	US-10-809-189-7331
16	14	77.8	25	9	US-10-809-189-7332
17	14	77.8	25	9	US-10-809-189-28185
18	14	77.8	25	9	US-10-956-157-202499
19	14	77.8	25	10	US-11-036-317-95923
20	13.8	76.7	25	8	US-10-719-900-151203
21	13.8	76.7	25	8	US-10-719-900-819413
22	13.8	76.7	25	8	US-10-719-900-971153
23	13.8	76.7	25	10	US-11-036-317-909425

25	10	US-11-036-317-939953	76.7	13.8	C 24
36	9	US-10-775-204-1955	76.7	13.8	C 25
36	9	US-10-775-204-1957	76.7	13.8	C 26
25	7	US-10-719-956-251026	74.4	13.4	C 27
25	7	US-10-719-956-590464	74.4	13.4	C 28
25	7	US-10-719-956-590971	74.4	13.4	C 29
25	10	US-11-036-317-260636	74.4	13.4	C 30
25	10	US-11-036-317-260637	74.4	13.4	C 31
44	6	US-10-181-808-2	74.4	13.4	C 32
44	6	US-10-488-428-6	74.4	13.4	C 33
63	3	US-09-908-975-2289	74.4	13.4	C 34
65	3	US-10-845-057-148	73.3	13.2	C 35
22	9	US-10-845-057-304	73.3	13.2	C 36
22	9	US-10-845-057-454	73.3	13.2	C 37
22	9	US-10-845-057-610	73.3	13.2	C 38
23	9	US-10-490-955-59	73.3	13.2	C 39
23	9	US-10-490-955-428	73.3	13.2	C 40
23	9	US-10-490-955-429	73.3	13.2	C 41
23	9	US-10-859-321-27	73.3	13.2	C 42
23	9	US-10-912-440-27	73.3	13.2	C 43
25	7	US-10-719-956-178396	73.3	13.2	C 44
25	7	US-10-719-956-253388	73.3	13.2	C 45
25	7	US-10-719-956-253389	73.3	13.2	C 46
25	7	US-10-719-956-538896	73.3	13.2	C 47
25	7	US-10-719-956-600309	73.3	13.2	C 48
25	7	US-10-719-956-633837	73.3	13.2	C 49
25	8	US-10-719-900-69529	73.3	13.2	C 50
25	8	US-10-719-900-169586	73.3	13.2	C 51
25	8	US-10-719-900-353891	73.3	13.2	C 52
25	8	US-10-719-900-353893	73.3	13.2	C 53
25	8	US-10-719-900-461964	73.3	13.2	C 54
25	8	US-10-719-900-587640	73.3	13.2	C 55
25	8	US-10-719-900-681173	73.3	13.2	C 56
25	8	US-10-719-900-852808	73.3	13.2	C 57
25	8	US-10-719-900-866359	73.3	13.2	C 58
25	8	US-10-719-900-978449	73.3	13.2	C 59
25	10	US-11-036-317-434317	73.3	13.2	C 60
25	10	US-11-036-317-466230	73.3	13.2	C 61
25	10	US-11-036-317-501487	73.3	13.2	C 62
25	10	US-11-036-317-801432	73.3	13.2	C 63
25	10	US-11-036-317-801432	73.3	13.2	C 64
25	10	US-11-036-317-829274	73.3	13.2	C 65
25	10	US-11-036-317-829274	73.3	13.2	C 66
68	6	US-10-204-884-1198	73.3	13.2	C 67
72	9	US-10-490-955-220	73.3	13.2	C 68
72	9	US-10-490-955-286	73.3	13.2	C 69
72	9	US-10-501-665-16	73.3	13.2	C 70
72	9	US-10-501-964-16	73.3	13.2	C 71
76	9	US-10-490-955-219	73.3	13.2	C 72
76	9	US-10-490-955-285	73.3	13.2	C 73
25	8	US-10-719-900-526705	72.2	13	C 74
25	8	US-10-719-900-546811	72.2	13	C 75
25	8	US-10-719-900-546811	72.2	13	C 76
25	10	US-11-036-317-81918	72.2	13	C 77
25	10	US-11-036-317-878822	72.2	13	C 78
25	10	US-11-036-317-906444	72.2	13	C 79
25	10	US-11-036-317-957208	72.2	13	C 80
25	10	US-11-036-317-983122	72.2	13	C 81
23	9	US-10-825-593-56	71.1	12.8	C 82
25	5	US-10-098-2638-14720	71.1	12.8	C 83
25	7	US-10-681-773-44439	71.1	12.8	C 84
25	7	US-10-681-773-48133	71.1	12.8	C 85
25	7	US-10-681-773-95190	71.1	12.8	C 86
25	7	US-10-719-956-241477	71.1	12.8	C 87
25	7	US-10-719-956-267497	71.1	12.8	C 88
25	7	US-10-719-956-468207	71.1	12.8	C 89
25	7	US-10-719-956-635311	71.1	12.8	C 90
25	7	US-10-719-956-635312	71.1	12.8	C 91
25	8	US-10-719-900-97857	71.1	12.8	C 92
25	8	US-10-719-900-98935	71.1	12.8	C 93
25	8	US-10-719-900-175637	71.1	12.8	C 94
25	8	US-10-719-900-231009	71.1	12.8	C 95
25	8	US-10-719-900-244281	71.1	12.8	C 96

Sequence 939953, Sequence 1955, Ap Sequence 1957, Ap Sequence 251026, Sequence 590464, Sequence 590971, Sequence 260636, Sequence 260637, Sequence 2, Appli Sequence 2, Appli Sequence 2289, Ap Sequence 148, App Sequence 304, App Sequence 454, App Sequence 610, App Sequence 59, Appl Sequence 428, App Sequence 429, App Sequence 27, Appl Sequence 27, Appl Sequence 178396, Sequence 253388, Sequence 253389, Sequence 538896, Sequence 600309, Sequence 633837, Sequence 69529, A Sequence 169586, Sequence 353891, Sequence 353893, Sequence 461964, Sequence 587640, Sequence 851173, Sequence 852808, Sequence 866359, Sequence 978449, Sequence 315918, Sequence 434317, Sequence 466230, Sequence 501487, Sequence 801432, Sequence 829274, Sequence 829274, Sequence 1198, Ap Sequence 126, App Sequence 220, App Sequence 286, App Sequence 16, Appl Sequence 219, App Sequence 219, App Sequence 285, App Sequence 526705, Sequence 546811, Sequence 546811, Sequence 20246, Sequence 81918, A Sequence 978822, Sequence 906444, Sequence 906444, Sequence 957208, Sequence 983122, Sequence 56, Appl Sequence 14720, A Sequence 44439, A Sequence 48133, A Sequence 95190, A Sequence 241477, Sequence 267497, Sequence 468207, Sequence 635311, Sequence 635312, Sequence 97857, A Sequence 98935, A Sequence 175637, Sequence 231009, Sequence 244281,

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97 12.8 71.1 25 8 US-10-719-900-346264 Sequence 346264,
98 12.8 71.1 25 8 US-10-719-900-393527 Sequence 393527,
99 12.8 71.1 25 8 US-10-719-900-393528 Sequence 393528,
c 100 12.8 71.1 25 8 US-10-719-900-437530 Sequence 437530,

ALIGNMENTS

RESULT 1
US-10-182-049-19
; Sequence 19, Application US/10182049
; Publication No. US20050113322A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSION
; FILE REFERENCE: RTSP-0360
; CURRENT APPLICATION NUMBER: US/10/182,049
; CURRENT FILING DATE: 2002-07-27
; PRIOR APPLICATION NUMBER: 09/490,208
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-182-049-19

Query Match 100.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAGA 18
| | | | | | | | | | | | | | | |
Db 1 CATCAAGGTGGCCGAGA 18

RESULT 2
US-10-719-900-244282
; Sequence 244282, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 244282
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-244282

Query Match 80.0%; Score 14.4; DB 8; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGGCCGAG 17
| | | | | | | | | | | | | |
Db 7 ATCAAGGTGGCTGAG 22

RESULT 3
US-11-036-317-138400/c
```

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; Sequence 138400, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 138400
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-138400

Query Match 80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGA 16
| | | | | | | | | | | | | |
Db 16 CTTCAAGGTGGCCGA 1

RESULT 4
US-11-036-317-203113
; Sequence 203113, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 203113
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-203113

Query Match 80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGGCCGAG 17
| | | | | | | | | | | | | |
Db 8 ATCAAGGTGGCCGAG 23

RESULT 5
US-11-036-317-231362
; Sequence 231362, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

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; SEQ ID NO 231362
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-231362

Query Match      80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATCAAAGGTGCCGAG 17
    ||||| ||||| |||||
Db 9 ATCAAAGGTGCCGAG 24

RESULT 6
US-11-036-317-270126
; Sequence 270126, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 270126
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-270126

Query Match      80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATCAAAGGTGCCGAG 17
    ||||| ||||| |||||
Db 5 ATCAAAGGTGCCGAG 20

RESULT 7
US-11-036-317-340096
; Sequence 340096, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 340096
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-340096

Query Match      80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATCAAAGGTGCCGAG 17
    ||||| ||||| |||||
Db 7 ATCAAAGGTGCCGAG 22

RESULT 8
US-11-036-317-364267/c
; Sequence 364267, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 364267
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-364267

Query Match      80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATCAAAGGTGCCGAG 16
    ||||| ||||| |||||
Db 16 CTTCAAAGGTGCCGAG 1

RESULT 9
US-11-036-317-365442
; Sequence 365442, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 365442
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-365442

Query Match      80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATCAAAGGTGCCGAG 17
    ||||| ||||| |||||
Db 4 ATCAAAGGTGCCGAG 19

RESULT 10
US-11-036-317-366373
; Sequence 366373, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13

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; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 366373
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-366373

Query Match 80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGCCGAG 17
Db 6 ATCAAGGTGCCGAG 21

RESULT 11

US-11-036-317-895040
; Sequence 895040, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 895040
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-895040

Query Match 80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGCCGAG 17
Db 9 ATCAAGGTGCCGAG 24

RESULT 12

US-11-036-317-957650
; Sequence 957650, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 957650
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-957650

Query Match 80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGCCGAG 17
Db 7 ATCAAGGTGCCGAG 22

RESULT 13
US-11-036-317-972134
; Sequence 972134, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 972134
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-972134

Query Match 80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGCCGAG 17
Db 4 ATCAAGGTGCCGAG 19

RESULT 14

US-11-036-317-972700
; Sequence 972700, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 972700
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-972700

Query Match 80.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGCCGAG 17
Db 6 ATCAAGGTGCCGAG 21

RESULT 15

US-10-809-189-7331/C
; Sequence 7331, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack

```

; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; PRIOR FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7331
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-7331

Query Match      77.8%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATCAAGGTGGCC 14
        |||||
DB      23 CATCAAGGTGGCC 10

RESULT 16
US-10-809-189-7332/c
; Sequence 7332, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7332
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-7332

Query Match      77.8%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATCAAGGTGGCC 14
        |||||
DB      17 CATCAAGGTGGCC 4

RESULT 17
US-10-809-189-28185
; Sequence 28185, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189

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; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28185
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-28185

Query Match      77.8%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 AAAGTGGCCGAGA 18
        |||||
DB      8 AAAGTGGCCGAGA 21

RESULT 18
US-10-956-157-202499/c
; Sequence 202499, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patent version 3.2
; SEQ ID NO 202499
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-202499

Query Match      77.8%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATCAAGGTGGCC 14
        |||||
DB      18 CATCAAGGTGGCC 5

RESULT 19
US-11-036-317-95923
; Sequence 95923, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 95923
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-95923

Query Match      77.8%; Score 14; DB 10; Length 25;

```

Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCC 14
| | | | | | | | | | | | | | | |
Db 3 CATCAAGGTGGCC 16

RESULT 20
US-10-719-900-151203/c
; Sequence 151203, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 151203
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-151203

Query Match 76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAG 17
| | | | | | | | | | | | | | | |
Db 22 CATCAAGGTGGCTAAG 6

RESULT 21
US-10-719-900-819413/c
; Sequence 819413, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 819413
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-819413

Query Match 76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAG 17
| | | | | | | | | | | | | | | |
Db 22 CATCAATTTGGCCGAG 6

RESULT 22
US-10-719-900-971153/c
; Sequence 971153, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 971153
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-971153

Query Match 76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGGCCGAGA 18
| | | | | | | | | | | | | | | |
Db 19 ATCAAGGTGGCACAGA 3

RESULT 23
US-11-036-317-909425/c
; Sequence 909425, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 909425
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-909425

Query Match 76.7%; Score 13.8; DB 10; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGGCCGAGA 18
| | | | | | | | | | | | | | | |
Db 20 AACAAAGTGGCACAGA 4

RESULT 24
US-11-036-317-939953/c
; Sequence 939953, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 939953
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-939953

Query Match	76.7%;	Score 13.8;	DB 10;	Length 25;
Best Local Similarity	88.2%;	Pred. No. 2.7e+03;		
Matches 15;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

QY 2 ATCAAAGGTGCCGAGA 18
| | | | | | | | | | | | | | | | | |
Db 22 AACAAAGGTGCCAGAGA 6

RESULT 25

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US-10-775-204-1955
; Sequence 1955, Application US/10775204
; Publication No. US2005018664A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, William A.
; APPLICANT: Balance, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1955
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-204-1955

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Query Match          76.7%; Score 13.8; DB 9; Length 36;
Best Local Similarity 88.2%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 2 ATCAAAGGTGCCGAGA 18
|||
Db 15 ATCAAAGGTGCCGTAGA 31

Search completed: March 3, 2006, 08:48:46
Job time : 223.11 secs

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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:35:12 ; Search time 97.8559 Seconds
(without alignments)
403.294 Million cell updates/sec

Title: US-10-655-801-19

Perfect score: 18

Sequence: 1 catcaaggtgcccagaga 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 11869656

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA New.*

1:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
2:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
4:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
5:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
6:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
7:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
8:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
9:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
10:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
11:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
12:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
13:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred., No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14	77.8	25	12	US-11-121-849-16738
C 2	14	77.8	25	12	US-11-121-849-16738
C 3	13.8	76.7	19	10	US-11-101-244-1487950
C 4	13.8	76.7	19	10	US-11-101-244-1487950
C 5	13.8	76.7	19	10	US-11-101-244-1487950
C 6	13.8	76.7	19	10	US-11-101-244-1487950
C 7	13.8	76.7	19	10	US-11-101-244-1487950
C 8	13.8	76.7	19	10	US-11-101-244-1487950
C 9	13.4	74.4	19	10	US-11-101-244-1487950
C 10	13.4	74.4	19	10	US-11-101-244-1487950
C 11	13.4	74.4	19	10	US-11-101-244-1487950
C 12	13.4	74.4	19	10	US-11-101-244-1487950
C 13	13.4	74.4	19	10	US-11-101-244-1487950
C 14	13.4	74.4	19	10	US-11-101-244-1487950
C 15	13.4	74.4	19	10	US-11-101-244-1487950
C 16	13.4	74.4	19	10	US-11-101-244-1487950
C 17	13.4	74.4	19	10	US-11-101-244-1487950
C 18	13.4	74.4	19	10	US-11-101-244-1487950
C 19	13.4	74.4	19	10	US-11-101-244-1487950
C 20	13.4	74.4	19	10	US-11-101-244-1487950

19	11	US-11-083-784-980471	Sequence 980471,
20	8	US-10-310-914A-280157	Sequence 280157,
21	8	US-10-310-914A-280052	Sequence 280052,
22	12	US-11-121-849-1487950	Sequence 1487950,
23	12	US-11-121-849-1487950	Sequence 1487950,
24	12	US-11-121-849-1487950	Sequence 1487950,
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93	12	US-11-121-849-1487950	Sequence 1487950,

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94 12.4 68.9 19 10 US-11-101-244-28799 Sequence 28799, A
95 12.4 68.9 19 10 US-11-101-244-28899 Sequence 28899, A
c 96 12.4 68.9 19 10 US-11-101-244-37910 Sequence 37910, A
c 97 12.4 68.9 19 10 US-11-101-244-37928 Sequence 37928, A
98 12.4 68.9 19 10 US-11-101-244-296983 Sequence 296983,
99 12.4 68.9 19 10 US-11-101-244-296989 Sequence 296989,
100 12.4 68.9 19 10 US-11-101-244-297040 Sequence 297040,

ALIGNMENTS

RESULT 1
US-11-121-849-16738/c
; Sequence 16738, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 16738
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-16738

Query Match 77.8%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCC 14
Db 16 CATCAAGGTGGCC 3

RESULT 2
US-11-121-849-31257/c
; Sequence 31257, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 31257
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-31257

Query Match 77.8%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCC 14
Db 16 CATCAAGGTGGCC 3

RESULT 3
US-11-121-849-16738/c
; Sequence 16738, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 16738
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-16738

Query Match 77.8%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCC 14
Db 16 CATCAAGGTGGCC 3
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US-11-101-244-1487950/c
; Sequence 1487950, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1487950
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1487950

Query Match 76.7%; Score 13.8; DB 10; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAG 17
Db 18 CATCAAGGTGGCTGAG 2

RESULT 4
US-11-101-244-1515236/c
; Sequence 1515236, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1515236
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1515236

Query Match 76.7%; Score 13.8; DB 10; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CATCAAGGTGGCCGAG 17
Db 18 CATCAAGGTGGCTGAG 2

RESULT 5
US-11-083-784-1487950/c
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Sequence 1487950, Application US/11083784
 Publication No. US20050245475A1
 GENERAL INFORMATION:
 APPLICANT: Dharmacon, Inc.
 APPLICANT: Khvorova, Anastasia
 APPLICANT: Reynolds, Angela
 APPLICANT: Leake, Devin
 APPLICANT: Marshall, William
 APPLICANT: Scaringe, Stephen
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/083,784
 CURRENT FILING DATE: 2005-03-18
 PRIOR APPLICATION NUMBER: US/10/714,333
 PRIOR FILING DATE: 2003-11-14
 PRIOR APPLICATION NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIOR APPLICATION NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 159191
 SOFTWARE: Proprietary
 SEQ ID NO 1487950
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-083-784-1487950

Query Match 76.7%; Score 13.8; DB 11; Length 19;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAG 17
 Db 18 CATCAAGGTGGCCGAG 2

RESULT 6
 US-11-083-784-1515236/c
 Sequence 1515236, Application US/11083784
 Publication No. US20050245475A1
 GENERAL INFORMATION:
 APPLICANT: Dharmacon, Inc.
 APPLICANT: Khvorova, Anastasia
 APPLICANT: Reynolds, Angela
 APPLICANT: Leake, Devin
 APPLICANT: Marshall, William
 APPLICANT: Scaringe, Stephen
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/083,784
 CURRENT FILING DATE: 2005-03-18
 PRIOR APPLICATION NUMBER: US/10/714,333
 PRIOR FILING DATE: 2003-11-14
 PRIOR APPLICATION NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIOR APPLICATION NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 159191
 SOFTWARE: Proprietary
 SEQ ID NO 1515236
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-083-784-1515236

Query Match 76.7%; Score 13.8; DB 11; Length 19;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAG 17
 Db 18 CATCAAGGTGGCCGAG 2

RESULT 7

US-11-121-849-234566
 Sequence 234566, Application US/11121849
 Publication No. US20050272080A1
 GENERAL INFORMATION:
 APPLICANT: John Palma
 TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded:
 FILE REFERENCE: 3684.1
 CURRENT APPLICATION NUMBER: US/11/121,849
 CURRENT FILING DATE: 2005-05-03
 PRIOR APPLICATION NUMBER: 60/567,949
 PRIOR FILING DATE: 2004-05-03
 NUMBER OF SEQ ID NOS: 673904
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO 234566
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapien
 US-11-121-849-234566

Query Match 76.7%; Score 13.8; DB 12; Length 25;
 Best Local Similarity 88.2%; Pred. No. 2.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAG 17
 Db 9 CCTCAAGGTGGCTGAG 25

RESULT 8

US-11-101-244-621129
 Sequence 621129, Application US/11101244
 Publication No. US20050246794A1
 GENERAL INFORMATION:
 APPLICANT: Dharmacon, Inc.
 APPLICANT: Khvorova, Anastasia
 APPLICANT: Reynolds, Angela
 APPLICANT: Leake, Devin
 APPLICANT: Marshall, William
 APPLICANT: Scaringe, Stephen
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 FILE REFERENCE: 13499US
 CURRENT APPLICATION NUMBER: US/11/101,244
 CURRENT FILING DATE: 2005-04-07
 PRIOR APPLICATION NUMBER: 60/502,050
 PRIOR FILING DATE: 2003-09-10
 PRIOR APPLICATION NUMBER: 60/426,137
 PRIOR FILING DATE: 2002-11-14
 NUMBER OF SEQ ID NOS: 159191
 SOFTWARE: Proprietary
 SEQ ID NO 621129
 LENGTH: 19
 TYPE: RNA
 ORGANISM: Homo sapiens
 US-11-101-244-621129

Query Match 74.4%; Score 13.4; DB 10; Length 19;
 Best Local Similarity 86.7%; Pred. No. 4.3e+02;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGTGGCCGAGA 18
 Db 4 CCAAGGUGGCCGAGA 18

RESULT 9

US-11-101-244-889148
 Sequence 889148, Application US/11101244
 Publication No. US20050246794A1
 GENERAL INFORMATION:
 APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 889148
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-889148

Query Match 74.4%; Score 13.4; DB 10; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18
| | | | | | | | | | | | | | | | | | | | |
Db 4 CAAAGGUGGCCGAGA 18

RESULT 10
US-11-101-244-889168
; Sequence 889168, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 889168
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-889168

Query Match 74.4%; Score 13.4; DB 10; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18
| | | | | | | | | | | | | | | | | | | | |
Db 1 CAAAGGUGGCCGAGA 15

RESULT 11
US-11-101-244-926191
; Sequence 926191, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 926191
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-926191

Query Match 74.4%; Score 13.4; DB 10; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18
| | | | | | | | | | | | | | | | | | | | |
Db 4 CCAAGGUGGCCGAGA 18

RESULT 12
US-11-101-244-956569
; Sequence 956569, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 956569
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-956569

Query Match 74.4%; Score 13.4; DB 10; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18
| | | | | | | | | | | | | | | | | | | | |
Db 4 CCAAGGUGGCCGAGA 18

RESULT 13
US-11-101-244-956596
; Sequence 956596, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela

```

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 956596
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-956596

```

```

Query Match 74.4%; Score 13.4; DB 10; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 4 CAAAGGTGCGCCGAGA 18
| | | | | | | | | |
Db 3 CCAAGGUGGCCGAGA 17
| | | | | | | |

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RESULT 14
US-11-101-244-980471
; Sequence 980471, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 980471
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-980471

```

```

Query Match 74.4%; Score 13.4; DB 10; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 4 CAAAGGTGCGCCGAGA 18
| | | | | | | | | |
Db 4 CCAAGGUGGCCGAGA 18
| | | | | | | |

```

```

RESULT 15
US-11-083-784-621129
; Sequence 621129, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

```

```

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 621129
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-621129

```

```

Query Match 74.4%; Score 13.4; DB 11; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 4 CAAAGGTGCGCCGAGA 18
| | | | | | | | | |
Db 4 CCAAGGUGGCCGAGA 18
| | | | | | | |

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```

RESULT 16
US-11-083-784-889148
; Sequence 889148, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 889148
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-889148

```

```

Query Match 74.4%; Score 13.4; DB 11; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 4 CAAAGGTGCGCCGAGA 18
| | | | | | | | | |
Db 4 CCAAGGUGGCCGAGA 18
| | | | | | | |

```

```

RESULT 17
US-11-083-784-889168
; Sequence 889168, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.

```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 889168
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-889168

Query Match 74.4%; Score 13.4; DB 11; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18
| | | | | : | | | | |
Db 1 CAAAGGUGGCCGAGA 15

RESULT 18

US-11-083-784-926191
; Sequence 926191, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 926191
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-926191

Query Match 74.4%; Score 13.4; DB 11; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18
| | | | | : | | | | |
Db 4 CCAAGGUGGCCGAGA 18

RESULT 19

US-11-083-784-956569
; Sequence 956569, Application US/11083784

; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 956569
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-956569

Query Match 74.4%; Score 13.4; DB 11; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18
| | | | | : | | | | |
Db 4 CCAAGGUGGCCGAGA 18

RESULT 20

US-11-083-784-956596
; Sequence 956596, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 956596
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-956596

Query Match 74.4%; Score 13.4; DB 11; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAGA 18
| | | | | : | | | | |
Db 3 CCAAGGUGGCCGAGA 17

```

RESULT 21
US-11-083-784-980471
; Sequence 980471, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 980471
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-980471

Query Match      74.4%; Score 13.4; DB 11; Length 19;
Best Local Similarity 86.7%; Pred. No. 4.3e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 CAAAGGTGGCCGAGA 18
      |||||:|||||
Db      4 CCAAGGUGGCCGAGA 18

RESULT 22
US-10-310-914A-582157
; Sequence 582157, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 582157
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-582157

Query Match      74.4%; Score 13.4; DB 8; Length 20;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CATCAAGGTGGCCG 15
      |||||:|||||
Db      1 CCUCAAGGUGGCCG 15

RESULT 23
US-10-310-914A-280052
; Sequence 280052, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac

```

```

; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 280052
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-280052

Query Match      74.4%; Score 13.4; DB 8; Length 23;
Best Local Similarity 86.7%; Pred. No. 4.4e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 CAAAGGTGGCCGAGA 18
      |||||:|||||
Db      7 CAGAGGUGGCCGAGA 21

RESULT 24
US-11-121-849-252474/c
; Sequence 252474, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 252474
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-252474

Query Match      74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 4.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CAAAGGTGGCCGAGA 18
      |||||:|||||
Db      18 CAAAGGTGGCCGAGA 4

RESULT 25
US-11-175-859-105506/c
; Sequence 105506, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105506
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-105506

```

Query Match 74.4%; Score 13.4; DB 12; Length 50;
 Best Local Similarity 82.4%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATCAAAGGTGGCCGAGA 18
 |||||:|||||
 Db 33 ATCAAAGRTGGCCTAAA 17

Search completed: March 3, 2006, 07:56:43
 Job time : 98.0559 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:25:53 ; Search time 984.737 Seconds
(without alignments)
855.220 Million cell updates/sec

Title: US-10-655-801-19

Perfect score: 18

Sequence: 1 catcaaggtgcccagaga 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 512758

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gss1:*

10: gb_gss2:*

11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.8	82.2	72	9	CC556903 CH240 464
2	13.8	76.7	58	3	BM434781 JRT13G10
3	13.4	74.4	43	10	CL982875 GC0098 TI
4	13.4	74.4	53	10	CG800410 1118012A0
5	13.4	74.4	60	10	CG726326 1118089E0
6	13.4	74.4	63	10	CG806795 1118074A0
7	13.4	74.4	69	10	CG806795 1118074A0
8	13.2	73.3	59	11	DMB426975
9	13.2	73.3	61	10	CG802312
10	12.8	71.1	53	9	AZ339975
11	12.8	71.1	64	1	AA646597 ve46e05.r
12	12.8	71.1	64	1	AI624617 te9b07.x
13	12.8	71.1	78	9	AZ621111
14	12.4	68.9	45	3	BJ016067
15	12.4	68.9	57	1	AV834194
16	12.4	68.9	71	10	CG591414
17	12.4	68.9	71	1	AW164603 se74a07.y
18	12.4	68.9	74	10	CG514254
19	12.4	68.9	77	10	CG510224
20	12.4	68.9	79	3	BP133993
21	12.2	67.8	29	10	CZ487115
22	12.2	67.8	31	9	BH850478

C 23	12.2	67.8	56	10	CZ483104
C 24	12.2	67.8	59	2	BG409364
C 25	12.2	67.8	63	10	CG575872
C 26	12.2	67.8	65	1	AA827028
C 27	12.2	67.8	66	2	BG116020
C 28	12.2	67.8	67	11	CR278093
C 29	12.2	67.8	74	10	CG729734
C 30	12.2	67.8	78	1	AI523075
C 31	12.2	67.8	78	2	BG910496
C 32	12.2	67.8	79	11	CR254716
C 33	12.2	67.8	80	10	CG527496
C 34	12.2	67.8	80	11	CR190533
C 35	12.2	66.7	50	1	AUI06266
C 36	12.2	66.7	55	9	AZ776193
C 37	12.2	66.7	60	6	CD944560
C 38	12.2	66.7	75	10	CG37827
C 39	12.2	66.7	76	8	H58746
C 40	11.8	65.6	39	9	AZ384591
C 41	11.8	65.6	40	10	AL766247
C 42	11.8	65.6	41	9	AZ410968
C 43	11.8	65.6	50	1	AUI02883
C 44	11.8	65.6	52	9	BH221325
C 45	11.8	65.6	52	9	BH626197
C 46	11.8	65.6	53	9	B00363
C 47	11.8	65.6	69	10	CM053729
C 48	11.8	65.6	70	11	CR162837
C 49	11.8	65.6	71	9	BH894176
C 50	11.8	65.6	76	1	AA457044
C 51	11.8	65.6	76	7	CV466027
C 52	11.8	65.6	76	10	BX895654
C 53	11.8	65.6	77	10	CM064212
C 54	11.8	65.6	79	1	AA223105
C 55	11.8	65.6	79	1	AA553236
C 56	11.6	64.4	37	10	CG712023
C 57	11.6	64.4	49	10	CG783969
C 58	11.6	64.4	50	1	AA717501
C 59	11.6	64.4	52	11	CR359266
C 60	11.6	64.4	53	10	CM135706
C 61	11.6	64.4	54	9	BH628620
C 62	11.6	64.4	55	1	AA572472
C 63	11.6	64.4	55	2	BE732284
C 64	11.6	64.4	57	9	B01965
C 65	11.6	64.4	59	1	AA283228
C 66	11.6	64.4	61	1	AI570241
C 67	11.6	64.4	65	8	W75049
C 68	11.6	64.4	65	9	AZ470048
C 69	11.6	64.4	66	9	AZ809396
C 70	11.6	64.4	69	8	CM571160
C 71	11.6	64.4	70	8	Z19901
C 72	11.6	64.4	70	9	BH906540
C 73	11.6	64.4	71	9	CC885346
C 74	11.6	64.4	73	6	CF652273
C 75	11.6	64.4	76	1	AI873248
C 76	11.6	64.4	77	10	AG189240
C 77	11.6	64.4	77	10	CM031050
C 78	11.6	64.4	79	1	AW420201
C 79	11.6	64.4	79	5	BO756208
C 80	11.6	64.4	79	11	CR359149
C 81	11.4	63.3	20	9	AZ964660
C 82	11.4	63.3	43	1	AV952014
C 83	11.4	63.3	43	10	CL211120
C 84	11.4	63.3	52	5	BX763192
C 85	11.4	63.3	58	1	AJ747306
C 86	11.4	63.3	60	10	CZ490547
C 87	11.4	63.3	61	10	CZ490549
C 88	11.4	63.3	66	8	DR038246
C 89	11.4	63.3	66	5	BQ586352
C 90	11.4	63.3	68	11	CR147982
C 91	11.4	63.3	69	10	CG509165
C 92	11.4	63.3	70	10	AL755545
C 93	11.4	63.3	71	9	BZ290183
C 94	11.4	63.3	72	9	BZ290481
C 95	11.4	63.3	73	9	BH847153

CZ483104	f00637-5p
BG409364	gb91e01.y
CG575872	OST210072
AA827028	nr89h10.s
BG116020	6023318007
CR278093	Reverse s
CG729734	1119114D0
AI523075	ar68b07.x
BG910496	602806182
CR254716	Reverse s
CG527496	OST105496
CR190533	Reverse s
AUI06266	AUI06266
AZ776193	2M0009G10
CD944560	RDK 47 Ge
CG37827	104_837_1
H58746	yr25h02_el_1
AZ384591	1M0142K09
AL766247	Arabidops
AZ410968	1M0183B17
AUI02883	AUI02883
BH221325	1006100F0
BH626197	1007112A1
B00363	CSRL-108d3-
CM053729	104_294_1
CR162837	Forward s
BH894176	3526_1_28
AA457044	aa38d02.s
CV466027	MdfrC3095
BX895654	Arabidops
CM064212	104_310_1
AA223105	zr0508.r
AA553236	vk89d12.s
CG712023	1119023G0
CG783969	01S0720-0
AA717501	vu22d09.r
CR359266	Arabidops
CM135706	104_520_1
BH628620	1007083H1
AA572472	v182d07.r
BE732284	601570267
B01965	CSRL-144A5-
AA283228	CJC007 HT
AI570241	to76G04.x
W75049	me52h08.r1
AZ470048	1M0283L20
AZ809396	2M0073E21
CM571160	TTE000293
Z19901	HSAAAAM P
BH906540	SALK_0338
CC885346	SALK_1469
CF652273	45-L02016
AI873248	wf41d06.x
AG189240	Pan trogl
CM031050	104_259_1
AW420201	fj88f06.y
BO756208	BEm05 SO
CR359149	Arabidops
AZ964660	2M0234M21
AV952014	AV952014
CL211120	W191D04 G
BX763192	BX763192
AJ747306	AJ747306
CZ490547	f07803-3p
CZ490549	f07804-3p
DR038246	BNE000002
BQ586352	F012395-0
CR147982	Forward s
CG509165	OSF0111
AL755545	Arabidops
BZ290183	SALK_0236
BZ290481	SALK_0239
BH847153	SALK_0135

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96 11.4 63.3 77 5 BU649191
97 11.4 63.3 77 10 CG490588
98 11.4 63.3 79 9 BH906286
c 99 11.4 63.3 80 3 BM098397
c 100 11.2 62.2 42 10 CZ476761

ALIGNMENTS

RESULT 1
CC556903
LOCUS
DEFINITION CH240_464F22.T7 CHORI-240 Bos taurus genomic clone CH240_464F22,
genomic survey sequence.
ACCESSION CC556903
VERSION CC556903.1 GI:31884266
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bos.
1 (bases 1 to 72)
Holt.R., Stott.J., Yang.G., Barber.S., Smalrus.D., Prabhu.A.-L.,
Tsai.M., Cloutier.A., Lee.D., Ginn.N., Olson.T., Mayo.M., Chiu.R.,
Butterfield.Y., Kirkpatrick.R., Liu.J., Guin.R., Chan.A., Chiu.R.,
Mathewson.C., Wye.N., Masson.A., Brown-John.M., Jones.S.,
Schein.J., Marra.M., de Jong.P., Keele.J.W. and Kappes.S.M.
Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
Unpublished (2003)
TITLE Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
JOURNAL
COMMENT Other_GSSs: CH240_464F22.TARBAC13P2
Contact: Rob Holt
Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bccsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering-information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 464 row: F column: 22
Seq primer: T7
Class: BAC ends.
FEATURES
source
Location/Qualifiers
1..72
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_464F22"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull Li Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN
Query Match 82.2%; Score 14.8; DB 9; Length 72;
Best Local Similarity 88.9%; Pred. No. 6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CATCAAGGTTGCCGAGA 18
|||||
Db 11 CATAAAGTGGCGCGAGA 28

RESULT 2
BM434781
LOCUS
DEFINITION BM434781 Bos taurus Reticulum #1 library Bos taurus cDNA, mRNA
sequence.
ACCESSION BM434781
VERSION BM434781.1 GI:18456503
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bos.
1 (bases 1 to 58)
Hansen.C., Fu.A., Meng.Y., Li.C., Okine.E., Senses.C.W.,
Gordon.P.M.K. and Moore.S.S.
Gene Expression Profiling of the Bovine Gastrointestinal Tract
Unpublished (2002)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
Email: stephen.moore@ualberta.ca
Insert Length: 58 Std Error: 0.00
POLYA=No.
FEATURES
source
Location/Qualifiers
1..58
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="Smooth muscle"
/cell_type="Stratified squamous epithelial"
/dev_stage="Young adult"
/lab_host="XLI-BlueMRF's strain"
/clone_lib="Bos taurus Reticulum #1 library"
/note="Organ: Reticulum; Vector: Uni-2ZAPXR; Site_1:
EcoRI; Site_2: Xho I"

ORIGIN
Query Match 76.7%; Score 13.8; DB 3; Length 58;
Best Local Similarity 88.2%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATCAAAGTGGCGCGAGA 18
|||||
Db 6 ATCAAAGTGGCGCGTGA 22

RESULT 3
CL982875/c
LOCUS
DEFINITION CL982875 TIGEM gene trap library Mus musculus cDNA clone 8322.18,
mRNA sequence.
ACCESSION CL982875
VERSION CL982875.1 GI:52420237
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 43)
Cobellis.G., Nicolaus.G., Iovino.M., Romito.A., Marra.E.,
Barbarisi.M., Sardiello.M., Di Giorgio.F.P., Iovino.N., Zollo.M.,
Ballabio.A. and Cortese.R.
Tagging genes with cassette-exchange sites
Nucleic Acids Res. 33 (4), e44 (2005)
15741177.
Contact: TIGEM
107

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TIGEM
Via P. Castellino, 111, 80131 NAPOLI, ITALY
Tel: +390816132205
Fax: +390815790919
Email: cobellis@tigem.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from TIGEM. Annotation information available from TIGEM
Class: Gene Trap.

FEATURES

source
Location/Qualifiers
1..43
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 ola"
/db_xref="taxon:10090"
/clone="8322.18"
/sex="male"
/cell_type="Embryonic stem cell"
/clone_lib="E14"
/clone_lib="TIGEM gene trap library"
/note="Vector: pFLIP1"

ORIGIN

Query Match 74.4%; Score 13.4; DB 10; Length 43;
Best Local Similarity 93.3%; Pred. No. 3.1e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGTGGCCGAGA 18
|||||
Db 38 CAAAGTGGCCGAGA 24

RESULT 4
CG800410
LOCUS
DEFINITION
1118012A01.1EL_x1 1118 - RescueMu Grid S Zea mays genomic, genomic survey sequence.
ACCESSION
CG800410
VERSION
CG800410.1 GI:38236196
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 53)
Walbot.V.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1118012 row: 25
Class: transposon-tagged.

FEATURES

source
Location/Qualifiers
1..53
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1118 - RescueMu Grid S"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 74.4%; Score 13.4; DB 10; Length 53;
Best Local Similarity 93.3%; Pred. No. 3.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATCAAAGTGGCGGA 16
|||||
Db 21 ATCAAAGTGGCGCA 35

RESULT 5

CG726326
LOCUS
DEFINITION
1119089E07.1EL_x1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.
ACCESSION
CG726326
VERSION
CG726326.1 GI:37764970
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 60)
Walbot.V.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119089 row: 11
Class: transposon-tagged.

FEATURES

source
Location/Qualifiers
1..60
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

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Query Match      74.4%; Score 13.4; DB 10; Length 60;
Best Local Similarity 93.3%; Pred. No. 3.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGCCGA 16
Db 16 ATCAAGGTGCCAA 30

RESULT 6
CG806795
LOCUS
DEFINITION 1118074A04.1BL x1 1118 - RescueMu Grid S Zea mays genomic, genomic
survey sequence.
ACCESSION CG806795
VERSION CG806795
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 63)
Walbot, V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1118074 row: 1
Class: transposon-tagged.
Class: transposon-tagged.
FEATURES
source
Location/Qualifiers
1..63
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1118 - RescueMu Grid S"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
sites. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid S was grown at San Diego in 2002. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

ORIGIN
Query Match      74.4%; Score 13.4; DB 10; Length 63;
Best Local Similarity 93.3%; Pred. No. 3.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGCCGA 16
Db 19 ATCAAGGTGCCAA 33

RESULT 7
CW020333/c
LOCUS

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GC0591 TIGEM gene trap library Mus musculus cDNA clone 9148.105,
mRNA sequence.
ACCESSION CW020333
VERSION CW020333.1 GI:52789593
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 69)
Cobellis, G., Nicolaus, G., Iovino, M., Romito, A., Marra, E.,
Barbarisi, M., Sardello, M., Di Giorgio, F.P., Iovino, N., Zollo, M.,
Ballabio, A. and Cortese, R.
Tagging genes with cassette-exchange sites
Nucleic Acids Res. 33 (4), e44 (2005)
15741177
Contact: TIGEM
107
TIGEM
Via P. Castellino, 111, 80131 NAPOLI, ITALY
Tel: +390816132205
Fax: +390815790919
Email: cobellis@tigem.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from TIGEM. Annotation information
available from TIGEM
Class: Gene Trap.
Location/Qualifiers
1..69
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Ola"
/db_xref="taxon:10090"
/clone="9148.105"
/sex="male"
/cell_type="Embryonic stem cell"
/cell_line="E14"
/clone_lib="TIGEM gene trap library"
/notes="Vector: pFLIP1"

ORIGIN
Query Match      74.4%; Score 13.4; DB 10; Length 69;
Best Local Similarity 93.3%; Pred. No. 3.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CAAAGTGGCCGAGA 18
Db 38 CAAAGTGGCCGAGA 24

RESULT 8
DME426975/c
LOCUS
DEFINITION Drosophila melanogaster X chromosomal sequence flanking P-lacW
insertion, strain 1(l)G0074, genomic survey sequence.
ACCESSION AJ426975
VERSION AJ426975.1 GI:18478196
KEYWORDS GSS; genome survey sequence.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1
Peter, A., Schottler, P., Werner, M., Beinert, N., Dowe, G., Burkert, P.,
Mourkioti, F., Denter, L., He, Y., Deak, P., Benos, P.V., Gatt, M.K.,
Murphy, L., Harris, D., Barrell, B., Ferraz, C., Vidal, S., Brun, C.,
Demalle, J., Cadieu, E., Dreano, S., Gloux, S., Lelaure, V.,
Mottier, S., Galibert, F., Borkova, D., Minana, B., Kafatos, F.C.,
Bolshakov, S., Siden-Kiamos, I., Papagiannakis, G., Spanos, L.,
Louis, C., Madueno, E., de Pablos, B., Modolell, J., Bucheton, A.,

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Callister, D., Campbell, L., Henderson, N.S., McMillan, P.J.,
Salles, C., Raic, E., Valenti, P., Saunders, R.D., Billaud, A.,
Fachter, U., Klapper, R., Janning, W., Glover, D.M., Ashburner, M.,
Bellen, H.J., Jackle, H. and Schafer, U.
Mapping and identification of essential gene functions on the X
chromosome of *Drosophila*
EMBO Rep. 3 (1), 34-38 (2002)
11751581
2 (bases 1 to 59)
Direct Submission
Submitted (03-DEC-2001) Schaefer U., Abt. Molekulare
Entwicklungsbiologie, Max-Planck-Institut fuer biophysikalische
Chemie, Am Fassberg 11, D-37077, GERMANY
P insertion putatively linked to X chromosomal lethality.
Location/Qualifiers
1. .59
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="1(1)G0074"
/db_xref="taxon:7227"
/chromosome="X"
/map="16D1-2"
/note="isolated by 5' inverse PCR"
52. .59
/notes="8 bp target duplication after P-lacW insertion"

Query Match 73.3%; Score 13.2; DB 11; Length 59;
Best Local Similarity 83.3%; Pred. No. 4.2e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAGA 18
|||||
46 CATCATCGGTGGCAGAGA 29

CG802312 61 bp DNA linear GSS 10-NOV-2003
1118029f10.2EL_x1 1118 - RescueMu Grid S Zea mays genomic, genomic
survey sequence.
CG802312
CG802312.1 GI:382338098
GSS.
1 (bases 1 to 61)
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1118029 row: 5
Class: transposon-tagged.
Location/Qualifiers
1. .61
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"

RESULT 9
CG802312/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 71.1%; Score 12.8; DB 9; Length 53;
Best Local Similarity 87.5%; Pred. No. 6.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ATCAAGGTGCCGAG 17
|||||||
Db 46 ATCAAGGTGCCGAG 31

RESULT 11

AA646597/c
LOCUS
DEFINITION 64 bp mRNA linear EST 28-OCT-1997
ve46e05.r1 Soares mammary gland NbMMG Mus musculus cDNA clone
IMAGE:821216 5' similar to TR:G677916 G677916 UBIQUITIN PROTEASE.
; mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AA646597.1 GI:2573026
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 64)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Stepcoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wyllie, F., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE
JOURNAL
COMMENT
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:489496

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.

FEATURES

source
1. .64
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:821216"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"

ORIGIN

Query Match 71.1%; Score 12.8; DB 1; Length 64;
Best Local Similarity 87.5%; Pred. No. 6.9e+04;

/clone lib="Soares mammary gland NbMMG"
/note="Organ: mammary gland; Vector: p7T3D-Pac
(Pharmacia) with a modified polylinker; Site: 1; Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCGCAATGGTGTGTGTGTGTGTGTGTGT
T 3'] double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

Query Match 71.1%; Score 12.8; DB 1; Length 64;
Best Local Similarity 87.5%; Pred. No. 6.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCAAGGTGCCGAGA 18
|||||||
Db 57 TCAAGGTGCCGAGA 42

RESULT 12

AI624617/c
LOCUS
DEFINITION 64 bp mRNA linear EST 22-APR-1999
t669b07.x1 NCI CGAP Kid8 Homo sapiens cDNA clone IMAGE:2233813 3'
similar to TR:Q16540 Q16540 L23-RELATED PROTEIN. ; contains element
MER26 repetitive element ; mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AI624617.1 GI:4649548
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 64)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES

source
1. .64
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2233813"
/tissue_type="renal cell tumor"
/lab_host="DH10B"
/clone lib="NCI CGAP Kid8"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.2 kb. Life Technologies catalog #: 11524-014"

```

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 ATCAAGGTGGCCGAG 17
    |||||
Db 38 ATCAAGGTGGCCAG 23

RESULT 13
AZ621111
LOCUS 78 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0454E08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0454E08 F, genomic survey sequence.
ACCESSION AZ621111
VERSION 1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,B.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0454 row: E column: 08
Seq primer: CGTGTAAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 78.
FEATURES
Location/Qualifiers
1..78
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0454E08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Query Match 71.1%; Score 12.8; DB 9; Length 78;

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```

Best Local Similarity 87.5%; Pred. No. 7.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 TCACAGGTGGCCGAGA 18
    |||||
Db 21 TCACAGGTGGCTGAGA 36

RESULT 14
BJ016067
LOCUS 45 bp mRNA linear EST 05-DEC-2001
DEFINITION BJ016067 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA008F01 3',
mRNA sequence.
ACCESSION BJ016067
VERSION 1
KEYWORDS EST.
SOURCE Oryzias latipes (Japanese medaka)
ORGANISM Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE
1 (bases 1 to 45)
AUTHORS Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
TITLE Medaka EST Project in Takeda's lab
JOURNAL Unpublished (2001)
COMMENT Contact: Tadaasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
Location/Qualifiers
1..45
/organism="Oryzias latipes"
/mol_type="mRNA"
/strain="Hd-r"
/db_xref="taxon:8090"
/clone="MF01SSA008F01"
/sex="mixture of female and male"
/tissue_type="whole embryo"
/dev_stage="segmentation stage 20 - 25"
/clone_lib="MF01SSA cDNA"
ORIGIN
Query Match 68.9%; Score 12.4; DB 3; Length 45;
Best Local Similarity 92.9%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CATCAAGGTGGCC 14
    |||||
Db 27 CATCTAAGGTGGCC 40

RESULT 15
AV834194
LOCUS 57 bp mRNA linear EST 09-MAY-2002
DEFINITION AV834194 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
vulgare shoots germination Hordeum vulgare subsp. vulgare cDNA
clone bags6915, mRNA sequence.
ACCESSION AV834194
VERSION 1
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
REFERENCE
1 (bases 1 to 57)
AUTHORS Sato,K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2001)

```

```

COMMENT
Contact: Kazuhiro Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kzsato@rib.okayama-u.ac.jp,
URL: http://www.rib.okayama-u.ac.jp/barley/
database: http://www.shigen.nig.ac.jp/barley/barley.html.

FEATURES
    source
        Location/Qualifiers
            1..57
                /organism="Hordeum vulgare subsp. vulgare"
                /mol_type="mRNA"
                /cultivar="Haruna Nijo"
                /sub_species="vulgare"
                /db_xref="taxon:112509"
                /clone="bags615"
                /tissue_type="shoots"
                /dev_stage="germination"
                /clone_lib="K. Sato unpublished cDNA library: Hordeum
                vulgare subsp. vulgare shoots germination"

ORIGIN
Query Match      68.9%; Score 12.4; DB 1; Length 57;
Best Local Similarity 86.7%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCAAAGTGGCCGAG 17
    |||||
Db 46 TCAAAGGTGACGAG 32

RESULT 16
CG591414
LOCUS
DEFINITION
OST245945 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST245945,
mRNA sequence.
ACCESSION
CG591414.1 GI:37399301
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 67)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., Beltrande-Rio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridlie, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
Key, B.W. Jr., Kipp, P., Kohlhaufl, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Spark, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
Contact: Zambrowicz BP
OmiBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene trap.
Location/Qualifiers
    source
        1..67
            /organism="Mus musculus"
            /mol_type="mRNA"
            /strain="129Sv/Ev"
            /db_xref="taxon:10090"
            /clone="OST245945"
            /cell_type="embryonic stem cell"
            /clone_lib="Mus musculus 129Sv/Ev"

ORIGIN
Query Match      68.9%; Score 12.4; DB 1; Length 71;
Best Local Similarity 92.9%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAG 17
    |||||
Db 27 CAAAGGTGGCAGAG 40

RESULT 17
AW164603
LOCUS
DEFINITION
Gm-cl023-397 5', mRNA sequence.
ACCESSION
AW164603
VERSION
AW164603.1 GI:6341717
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 71)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Corvelli, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Other ESTs: BB822937 corresponding to Gm-r1070-7396 (3')
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57066 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 51.
Location/Qualifiers
    source
        1..71
            /organism="Glycine max"
            /mol_type="mRNA"
            /cultivar="r157"
            /db_xref="taxon:3847"
            /clone="GENOME SYSTEMS CLONE ID: Gm-cl023-397"
            /tissue_type="seed coats of greenhouse grown plants"
            /lab_host="DH10B"
            /clone_lib="Gm-cl023"
            /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
            cDNA library was constructed from mRNA isolated from seed
            coats (100-200mgs) of greenhouse grown plants. The
            library was prepared using the Life Technologies
            SuperScript cDNA library construction kit. Complementary
            DNA was synthesized from mRNA using a poly (dT) sequence
            with a Not I restriction site. Sal I linkers adapers
            were ligated to the blunt-ended cDNA fragments followed by
            Not I digestion. The cDNA fragments were directionally
            cloned into the Not I-Sal I restriction site of the
            pSPORT1 vector. The ligated cDNA fragments were
            transformed into E.coli Electromax DH10B host cells. This
            library was constructed by Dr. Lila Vodkin and Dr. Anu
            Khanna."

ORIGIN
Query Match      68.9%; Score 12.4; DB 1; Length 71;

```



```

Best Local Similarity 92.9%; Pred. No. 1.1e+05; Mismatches 1; Indels 0; Gaps 0;
Matches 13; Conservative 0;

QY 4 CAAAGGTGGCCGAG 17
    |||||
Db 19 CAAAGGTGGCCGAG 32
    |||||

RESULT 18
CG514254 74 bp mRNA linear GSS 01-OCT-2003
OST67986 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST67986,
mRNA sequence.
CG514254
CG514254.1 GI:37300827
GSS.
Mus musculus (house mouse)
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 74)
REFERENCE
AUTHORS
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnki kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
CONTACT: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES
source
Location/Qualifiers
1..74
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST67986"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
ORIGIN
Query Match 68.9%; Score 12.4; DB 10; Length 74;
Best Local Similarity 92.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAG 17
    |||||
Db 37 CAAAGGTGGCCGAG 50
    |||||

RESULT 19
CG510224 77 bp mRNA linear GSS 01-OCT-2003
OST61835 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST61835,
mRNA sequence.
CG510224
CG510224.1 GI:37294274
GSS.
Mus musculus (house mouse)
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 77)
REFERENCE
AUTHORS
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnki kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
CONTACT: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES
source
Location/Qualifiers
1..74
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST67986"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
ORIGIN
Query Match 68.9%; Score 12.4; DB 10; Length 74;
Best Local Similarity 92.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAG 17
    |||||
Db 37 CAAAGGTGGCCGAG 50
    |||||

RESULT 20
BPI33993/3 79 bp mRNA linear EST 05-NOV-2004
MAT001 Nicotiana tabacum cDNA clone BY6321, mRNA sequence.
BPI33993
BPI33993.1 GI:32876878
EST.
Nicotiana tabacum (common tobacco)
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 79)
REFERENCE
AUTHORS
Matsuoka,K., Demura,T., Galis,I., Horiguchi,T., Sasaki,M.,
Tashiro,G. and Fukuda,H.
A Comprehensive Gene Expression Analysis Toward the Understanding
of Growth and Differentiation of Tobacco BY-2 Cells
Plant Cell Physiol. 45 (9), 1280-1289 (2004)
15509851
CONTACT: Ken Matsuoka
Morphogenesis Research Group
RIKEN Plant Science Center
1-7-2 Suehirocho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9575
Fax: 81-45-503-9573
Email: by2@psc.riken.go.jp, URL:http://mrq.psc.riken.go.jp/strc/
The cDNA library was constructed from mRNA isolated from lag (9 h),
log (72 h) and stationary (7 days) old BY-2 cells.
FEATURES
source
Location/Qualifiers
1..79
/organism="Nicotiana tabacum"
/mol_type="mRNA"

```

```

Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 77)
REFERENCE
AUTHORS
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnki kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
CONTACT: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES
source
Location/Qualifiers
1..77
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST61835"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
ORIGIN
Query Match 68.9%; Score 12.4; DB 10; Length 77;
Best Local Similarity 92.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CAAAGGTGGCCGAG 17
    |||||
Db 38 CAAAGGTGGCCGAG 51
    |||||

RESULT 20
BPI33993/3 79 bp mRNA linear EST 05-NOV-2004
MAT001 Nicotiana tabacum cDNA clone BY6321, mRNA sequence.
BPI33993
BPI33993.1 GI:32876878
EST.
Nicotiana tabacum (common tobacco)
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 79)
REFERENCE
AUTHORS
Matsuoka,K., Demura,T., Galis,I., Horiguchi,T., Sasaki,M.,
Tashiro,G. and Fukuda,H.
A Comprehensive Gene Expression Analysis Toward the Understanding
of Growth and Differentiation of Tobacco BY-2 Cells
Plant Cell Physiol. 45 (9), 1280-1289 (2004)
15509851
CONTACT: Ken Matsuoka
Morphogenesis Research Group
RIKEN Plant Science Center
1-7-2 Suehirocho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9575
Fax: 81-45-503-9573
Email: by2@psc.riken.go.jp, URL:http://mrq.psc.riken.go.jp/strc/
The cDNA library was constructed from mRNA isolated from lag (9 h),
log (72 h) and stationary (7 days) old BY-2 cells.
FEATURES
source
Location/Qualifiers
1..79
/organism="Nicotiana tabacum"
/mol_type="mRNA"

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/cultivar="Bright Yellow No.2"
/db xref="taxon:4097"
/clone="BY6321"
/cell_line="BY-2"
/clone_lib="WAT001"
/note="Vector: pCEM-T easy; primer: M13 forward; mRNA
obtained from lag, log and stationary phase cells"

ORIGIN
Query Match      68.9%; Score 12.4; DB 3; Length 79;
Best Local Similarity 92.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AAAGTGGCCGAGA 18
    ||||| |||||
Db 45 AAAGGTAGCCGAGA 32

RESULT 21
CZ487115/c
LOCUS      CZ487115          29 bp      DNA      linear      GSS 29-APR-2005
DEFINITION f04573-Sprine Exelixis piggyBac WH insertions Drosophila
            melanogaster genomic Sequence recovered from 5' end of piggyBac,
            genomic survey sequence.
ACCESSION  CZ487115
VERSION     CZ487115.1 GI:62984553
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM    Drosophila melanogaster
REFERENCE   1 (bases 1 to 29)
AUTHORS     Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,
            Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,
            Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,
            Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K.,
            Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,
            Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,
            Swimmer,C., Kopczyński,C., Duyk,G., Winberg,M.L. and Margolis,J.
            A complementary transposon tool kit for Drosophila melanogaster
            using P and piggyBac
            Nat. Genet. 36 (3), 283-287 (2004)
JOURNAL     14981521
PUBMED
COMMENT     Contact: Roger A Hoskins
            Berkeley Drosophila Genome Project
            Lawrence Berkeley National Laboratory
            Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
            Tel: 510 486 4015
            Fax: 510 486 6798
            Email: Rhoskins@lbl.gov
            Sequence recovery method was inverse PCR.
            Sequence orientation is forward strand relative to 5' end of
            piggyBac element.
            The piggyBac insertion position is 26 in the 29 bases. This
            insertion position refers to the first base of the 4 base TTAA
            target recognition sequence.
            Class: transposon insertion site.
            Location/Qualifiers
                1..29
                /organism="Drosophila melanogaster"
                /mol_type="genomic DNA"
                /strain="isogenic w- strain"
                /db xref="taxon:7227"
                /clone_lib="Exelixis piggyBac WH insertions"
                /note="Vector: piggyBac WH (GenBank accession number
                AV515148); An isogenic w- Drosophila melanogaster strain
                was mutagenized by remobilization of transposable
                elements. We remobilized the WH element using the
                constitutive alpha-1 tubulin:piggyBac transposase source.
                We remobilized the WH element from a single ammunition
                element on the Binsinsy balancer chromosome in dysgenic
                females. We outcrossed dysgenic virgins females in vials to

```

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the isogenic w- strain and selected new hops in the
following generation. All lines were mapped to a
chromosome by standard genetic methods, examined for
homozygous viability, and used for recovery of flanking
genomic sequence by inverse PCR."

ORIGIN
Query Match      67.8%; Score 12.2; DB 10; Length 29;
Best Local Similarity 82.4%; Pred. No. 1.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATCAAGGTGGCCGAGA 18
    ||||| |||||
Db 19 ACCNATGGTGGCCAGA 3

RESULT 22
BH850478
LOCUS      BH850478          31 bp      DNA      linear      GSS 13-JUN-2002
DEFINITION SALK_071331.38.75.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_071331.38.75.x, genomic
            survey sequence.
ACCESSION  BH850478
VERSION     BH850478.1 GI:21421349
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
REFERENCE   1 (bases 1 to 31)
AUTHORS     Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,W., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmermann,J. and Ecker,J.R.
            A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
            Unpublished (2001)
JOURNAL
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
            Location/Qualifiers
                1..31
                /organism="Arabidopsis thaliana"
                /mol_type="genomic DNA"
                /ecotype="Col-0"
                /db xref="taxon:3702"
                /clone="SALK_071331.38.75.x"
                /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                /note="PCR was performed on Arabidopsis thaliana lines
                each of which contains one or more TDNA insertion
                elements. The resultant fragment for each line was
                directly sequenced to determine the genomic sequence at
                the site of insertion. Details of the protocols used can
                be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      67.8%; Score 12.2; DB 9; Length 31;
Best Local Similarity 82.4%; Pred. No. 1.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATCAAGGTGGCCGAG 17
    ||||| |||||
Db 1 CATCAACCGTGGCCGAG 17

RESULT 23

```

CZ483104/c
LOCUS
DEFINITION
CZ483104 56 bp DNA linear GSS 29-APR-2005
f00637-5prime Exelixis piggyBac WH insertions Drosophila
melanogaster genomic Sequence recovered from 5' end of piggyBac,
genomic survey sequence.
CZ483104
CZ483104.1 GI:62980542
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 56)
Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,
Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L.,
Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W.,
Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Kilpack, K.,
Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C.,
Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F.,
Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M.L. and Margolis, J.
A complementary transposon tool kit for Drosophila melanogaster
using P and piggyBac
Nat. Genet. 36 (3), 283-287 (2004)
14981521
Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of
piggyBac element.
The piggyBac insertion position is 53 in the 56 bases. This
insertion position refers to the first base of the 4 base TTA
target recognition sequence.
Class: transposon insertion site.
Location/Qualifiers
1..56
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_lib="Exelixis piggyBac WH insertions"
/note="Vector: piggyBac WH (GenBank accession number
AY15148); An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. We remobilized the WH element using the
constitutive alpha-1 tubulin:piggyBac transposase source.
We remobilized the WH element from a single amnion
element on the Binsyncy balancer chromosome in dysgenic
females. We outcrossed dysgenic virgin females in vials to
the isogenic w- strain and selected new hops in the
following generation. All lines were mapped to a
chromosome by standard genetic methods, examined for
homologous viability, and used for recovery of flanking
genomic sequence by inverse PCR."
ORIGIN
Query Match 67.8%; Score 12.2; DB 10; Length 56;
Best Local Similarity 82.4%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CATCAAGGTGGCCGAG 17
||||| |||||
Db 26 CATCAAAAGTGGTCCAG 10
RESULT 24
BG409364/c
LOCUS
DEFINITION
gb91e01.y1 Moss EST library PPG Physcomitrella patens cDNA clone
PEP SOURCE ID:PPG_CopyA-130902 5', mRNA sequence.
BG409364
BG409364.1 GI:13315709
EST.
Physcomitrella patens
Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 59)
Quatrano, R., Bashardes, S., Cove, D., Cumming, A., Knight, C.,
Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T.,
Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E.,
Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
Leeds/Wash U Moss EST Project
Unpublished (1999)
Contact: Ralph Quatrano
Leeds/Wash U Moss EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Libraries were constructed by Dr. Stavros Bashardes as part of the
Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
Putative full length read
vector to vector length is 60
Seq primer: -40RP from Gibco.
Location/Qualifiers
1..59
/organism="Physcomitrella patens"
/mol_type="mRNA"
/db_xref="taxon:3218"
/clone="PEP SOURCE ID:PPG_CopyA-130902"
/tissue_type="gametophore: 30 day old tissue,
ammonium-grown"
/lab_host="DH10B"
/clone_lib="Moss EST library PPG"
/note="Vector: pAMP1; Construction of the cDNA library was
performed by Dr. W. Gregg Clark using a modification of
the cDNA synthesis protocol developed in the laboratory of
Dr. Michael Lovett by Dr. Yulia Korshunova (personal
communication). First polyA + RNA was isolated from total
gametophore RNA using oligo dt magnetic beads. Following
this, first strand cDNA synthesis was performed on the
bead-bound polyA + RNA, during which an oligonucleotide
anchor sequence was incorporated onto the 5'-ends of the
cDNA. PCR amplification was then used to synthesize the
second strand, to amplify the double stranded DNA, and to
incorporate dUTP containing sequences into the ends of the
double stranded cDNA. This DNA was size selected and
cloned into pAMP1 using the CloneAMP pAMP1 System (Life
Technologies, GibcoBRL) for cloning amplification products
by a non-restriction site dependant process. The cloning
was directional based on sequence asymmetry introduced at
the ends during PCR amplification. The 3' cDNA ends are
proximal to the NotI site of the multiple cloning site in
pAMP1. This annealing mixture was transformed into
chemically competent DH10B cells and selected for
ampicillin resistant growth. The resulting clones (about
330,000) were pooled to make the library."
ORIGIN
Query Match 67.8%; Score 12.2; DB 2; Length 59;
Best Local Similarity 82.4%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CATCAAGGTGGCCGAG 17
||||| |||||

Db 44 CCTCAAAGATGCCGTG 28

RESULT 25
CG575872/c
LOCUS
DEFINITION CG575872 63 bp mRNA linear GSS 02-OCT-2003
OST210072 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST210072,
mRNA sequence.
ACCESSION CG575872
VERSION CG575872.1 GI:37366209
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 63)
AUTHORS Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
PUBMED 14610273
COMMENT Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES
source Location/Qualifiers
1..63
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST210072"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
ORIGIN
Query Match 67.8%; Score 12.2; DB 10; Length 63;
Best Local Similarity 82.4%; Pred. No. 1.4e+05;
Matches 14, Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CATCAAAGGTGGCGGAG 17
||| ||||| |||||
Db 17 CATGAAAGGGGGCGCG 1
Search completed: March 3, 2006, 11:01:24
Job time : 990.737 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:16:16 ; Search time 376.932 Seconds
(without alignments)
2714.499 Million cell updates/sec

Title: US-10-655-801-20

Perfect score: 18

Sequence: 1 ctgcttagaactgcccag 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5881141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2389942

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.8	76.7	65	6	CQ557748 Sequence
2	13.4	74.4	20	6	AX298577 Sequence
3	13.4	74.4	30	6	AX528800 Sequence
4	13.4	74.4	60	6	CQ547222 Sequence
5	13.2	73.3	37	6	BD181212 Sequence
6	13.2	73.3	37	6	AX522090 Sequence
7	13.2	73.3	53	6	I32831 Sequence 13
8	13.2	73.3	60	6	CQ538595 Sequence
9	13.2	73.3	60	6	CQ543182 Sequence
10	13.2	73.3	62	6	I32833 Sequence 15
11	13.2	73.3	65	6	AX083959 Sequence
12	13.2	73.3	65	6	CQ557381 Sequence
13	13.2	73.3	65	6	CQ559197 Sequence
14	13	72.2	70	6	E14578 DNA encodin
15	13	72.2	70	6	E14579 DNA encodin
16	12.8	71.1	17	6	AX273086 Sequence
17	12.8	71.1	18	6	BD104284 Kit and m
18	12.8	71.1	18	6	BD104285 Kit and m

BD106033 Novel LDL	20	6	BD106033	71.1	19
AR305122 Sequence	20	6	AR305122	71.1	20
AR309226 Sequence	20	6	AR309226	71.1	21
BD251172 Functiona	23	6	BD251172	71.1	22
AX712114 Sequence	28	6	AX712114	71.1	23
AR489327 Sequence	38	6	AR489327	71.1	24
CQ007942 Sequence	51	6	CQ007942	71.1	25
AX117897 Sequence	51	6	AX117897	71.1	26
CQ542693 Sequence	60	6	CQ542693	71.1	27
CQ548019 Sequence	60	6	CQ548019	71.1	28
CQ550743 Sequence	60	6	CQ550743	71.1	29
AX331527 Sequence	15	6	AX331527	68.9	30
CQ801000 Sequence	27	6	CQ801000	68.9	31
AR288675 Sequence	47	6	AR288675	68.9	32
CQ003044 Sequence	51	6	CQ003044	68.9	33
Z69472 H.sapiens m	57	8	HSTRK3X2	68.9	34
AX5935 Sequence 85	21	6	AX5935	67.8	35
AX003322 Sequence	21	6	AX003322	67.8	36
BD101757 Prolactin	27	6	BD101757	67.8	37
BD171936 Prolactin	27	6	BD171936	67.8	38
E43669 Novel G pro	27	6	E43669	67.8	39
AR650812 Sequence	29	6	AR650812	67.8	40
AX792539 Sequence	30	6	AX792539	67.8	41
AX613041 Sequence	50	6	AX613041	67.8	42
AX613043 Sequence	50	6	AX613043	67.8	43
AX613045 Sequence	50	6	AX613045	67.8	44
AX613046 Sequence	50	6	AX613046	67.8	45
CQ536228 Sequence	60	6	CQ536228	67.8	46
CQ548094 Sequence	60	6	CQ548094	67.8	47
CQ549114 Sequence	60	6	CQ549114	67.8	48
CQ562630 Sequence	60	6	CQ562630	67.8	49
AR126060 Sequence	62	6	AR126060	67.8	50
CQ532194 Sequence	65	6	CQ532194	67.8	51
CQ556366 Sequence	65	6	CQ556366	67.8	52
CQ557526 Sequence	65	6	CQ557526	67.8	53
AR055468 Sequence	22	6	AR055468	66.7	54
AX600785 Sequence	22	6	AX600785	66.7	55
AR138974 Sequence	30	6	AR138974	66.7	56
I44864 Sequence 4	30	6	I44864	66.7	57
AR208296 Sequence	30	6	AR208296	66.7	58
CQ760652 Sequence	39	6	CQ760652	66.7	59
I83409 Sequence 10	40	6	I83409	66.7	60
CQ537842 Sequence	60	6	CQ537842	66.7	61
CQ539418 Sequence	60	6	CQ539418	66.7	62
AX486602 Sequence	65	6	AX486602	66.7	63
AR329566 Sequence	16	6	AR329566	65.6	64
AR188282 Sequence	17	6	AR188282	65.6	65
AR324115 Sequence	17	6	AR324115	65.6	66
AR328730 Sequence	17	6	AR328730	65.6	67
AR597575 Sequence	17	6	AR597575	65.6	68
AX273327 Sequence	17	6	AX273327	65.6	69
CQ840020 Sequence	20	6	CQ840020	65.6	70
BD274871 NOVEL POL	24	6	BD274871	65.6	71
AX528497 Sequence	24	6	AX528497	65.6	72
BD136232 Novel gen	27	6	BD136232	65.6	73
AR264642 Sequence	27	6	AR264642	65.6	74
AR474926 Sequence	28	6	AR474926	65.6	75
AR567958 Sequence	28	6	AR567958	65.6	76
AX555702 Sequence	28	6	AX555702	65.6	77
AX698702 Sequence	28	6	AX698702	65.6	78
AX339255 Sequence	29	6	AX339255	65.6	79
AR011115 Sequence	30	6	AR011115	65.6	80
AR038274 Sequence	30	6	AR038274	65.6	81
AR049415 Sequence	30	6	AR049415	65.6	82
AR075204 Sequence	30	6	AR075204	65.6	83
AR152616 Sequence	30	6	AR152616	65.6	84
I58563 Sequence 28	30	6	I58563	65.6	85
I61228 Sequence 35	30	6	I61228	65.6	86
I86667 Sequence 7	30	6	I86667	65.6	87
AR219325 Sequence	30	6	AR219325	65.6	88
AR238456 Sequence	30	6	AR238456	65.6	89
AR367618 Sequence	30	6	AR367618	65.6	90
AR455480 Sequence	30	6	AR455480	65.6	91

c 92 11.8 65.6 30 6 AX323297 Sequence
 93 11.8 65.6 33 6 AX061516 Sequence
 94 11.8 65.6 34 6 BD218022 Sequence
 95 11.8 65.6 34 6 AR274248 Sequence
 96 11.8 65.6 38 6 BD140801 Sequence
 97 11.8 65.6 38 6 BD140952 Monitorin
 98 11.8 65.6 42 6 AR126195 Sequence
 99 11.8 65.6 42 6 AR126196 Sequence
 100 11.8 65.6 42 6 AR126197 Sequence

ALIGNMENTS

RESULT 1
 CQ557748
 LOCUS AX323297 65 bp DNA linear PAT 30-JAN-2004
 DEFINITION Sequence 27383 from Patent WO0210449.
 ACCESSION CQ557748
 VERSION CQ557748.1 GI:41524175
 KEYWORDS Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 REFERENCE 1 Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
 Oligonucleotide library for detecting rna transcripts and splice
 variants that populate a transcriptome
 Patent: WO 0210449-A 27383 07-FEB-2002;
 Compugen Inc. (US)
 FEATURES Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:10090"

ORIGIN

Query Match 76.7%; Score 13.8; DB 6; Length 65;
 Best Local Similarity 88.2%; Pred. No. 4.9e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCCA 17
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 Db 18 CTGCTTGCCTGCCCA 34

RESULT 2
 AX298577
 LOCUS AX298577 20 bp DNA linear PAT 26-NOV-2001
 DEFINITION Sequence 211 from Patent WO0183749.
 ACCESSION AX298577
 VERSION AX298577.1 GI:17128567
 KEYWORDS Mus sp.
 ORGANISM Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 Bachmanov,A.A., Beauchamp,G.K., Chatterjee,A., de Jong,P.J., Li,S.,
 Li,X., Ohmen,J.D., Reed,D.R., Ross,D. and Tordoff,M.G.
 TITLE Gene and sequence variation associated with sensing carbohydrate
 compounds and other sweeteners
 JOURNAL Patent: WO 0183749-A 211 08-NOV-2001;
 WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center
 (US)

FEATURES Location/Qualifiers
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 /organism="Mus sp."
 /mol_type="unassigned DNA"
 /db_xref="taxon:10095"

ORIGIN

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 Best Local Similarity 93.3%; Pred. No. 8e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CTGCTAGAACTGCC 15
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 Db 4 CTGCTAGAACTGCC 18

RESULT 3
 AX528800
 LOCUS AX528800 30 bp DNA linear PAT 21-NOV-2002
 DEFINITION Sequence 49 from Patent WO02059357.
 ACCESSION AX528800
 VERSION AX528800.1 GI:25172855
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1 Pedersen,M.L.
 AUTHORS Assay and kit for analyzing gene expression
 TITLE Patent: WO 02059357-A 49 01-AUG-2002;
 JOURNAL Location/Qualifiers
 FEATURES source
 1..30
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="synthetic construct"

ORIGIN

Query Match 74.4%; Score 13.4; DB 6; Length 30;
 Best Local Similarity 93.3%; Pred. No. 8.2e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 TCTAGAACTGCCCAAG 18
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 Db 3 TCTAGAACTGCCCAAG 17

RESULT 4

CQ547222/c
 LOCUS CQ547222 60 bp DNA linear PAT 30-JAN-2004
 DEFINITION Sequence 16857 from Patent WO0210449.
 ACCESSION CQ547222
 VERSION CQ547222.1 GI:41513486
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
 AUTHORS Oligonucleotide library for detecting rna transcripts and splice
 TITLE variants that populate a transcriptome
 JOURNAL Patent: WO 0210449-A 16857 07-FEB-2002;
 Compugen Inc. (US)
 FEATURES Location/Qualifiers
 source
 1..60
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 74.4%; Score 13.4; DB 6; Length 60;
 Best Local Similarity 93.3%; Pred. No. 8.6e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 TCTAGAACTGCCCAAG 18
 |||||

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Db      16  TCTAGAACTGCTCCAG 2
RESULT 5
LOCUS   BD181212
DEFINITION Expression-regulatory sequence.
ACCESSION BD181212
VERSION   BD181212.1 GI:30792130
KEYWORDS JP 2002320495-A/12.
SOURCE   synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 37)
AUTHORS Mashko,S.V. and Zimenkov,D.V.
TITLE Expression-regulatory sequence
JOURNAL Patent: JP 2002320495-A 12 05-NOV-2002;
COMMENT AJINOMOTO CO INC
OS Artificial Sequence
PN JP 2002320495-A/12
PD 05-NOV-2002
PF 22-FEB-2002 JP 2002046910
PI 22-FEB-2001 RU 2001104817
PR SERGEI VLADIMIROVICH MASHKO, DANILA VADIMOVICH ZIMENKOV PC
CI2N15/09, CI2N9/10//CI2N1/21, (CI2N1/21, CI2R1/19), CI2N15/00 CC
Primer
FH Key Location/Qualifiers
FT source 1..47
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source Location/Qualifiers
1..37 /organism="Artificial Sequence".
1..37 /organism="synthetic construct"
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/db_xref="taxon:32630"
ORIGIN
Query Match 73.3%; Score 13.2; DB 6; Length 37;
Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCG 18
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Db 4 CTGCTAGAACTGCTACAG 21

RESULT 6
AX522090
LOCUS   AX522090
DEFINITION Sequence 12 from Patent EP1234883.
ACCESSION AX522090
VERSION   AX522090.1 GI:24410975
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Mashko,S.V. and Zimenkov,D.V.
TITLE Expression control sequence
JOURNAL Patent: EP 1234883-A 12 28-AUG-2002;
COMMENT Ajinomoto Co., Inc. (JP)
FEATURES
source Location/Qualifiers
1..37 /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"
ORIGIN
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Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCG 18
|||||
Db 4 CTGCTAGAACTGCTACAG 21

RESULT 7
LOCUS   I32831
DEFINITION Sequence 13 from patent US 5589364.
ACCESSION I32831
VERSION   I32831.1 GI:1823622
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 53)
AUTHORS Williams,J.I., Pierce,J.C., Anderson,G.Mark. and Kari,P.
TITLE Recombinant production of biologically active peptides and proteins
JOURNAL Patent: US 5589364-A 13 31-DEC-1996;
COMMENT Location/Qualifiers
1..53 /organism="unassigned DNA"
/mol_type="unassigned DNA"
ORIGIN
Query Match 73.3%; Score 13.2; DB 6; Length 53;
Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCG 18
|||||
Db 15 CTGCTAGAACTGCTAAG 32

RESULT 8
CQ538595
LOCUS   CQ538595
DEFINITION Sequence 8230 from Patent WO0210449.
ACCESSION CQ538595
VERSION   CQ538595.1 GI:41504859
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 8230 07-FEB-2002;
COMMENT Compugen Inc. (US)
FEATURES
source Location/Qualifiers
1..60 /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 73.3%; Score 13.2; DB 6; Length 60;
Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCG 18
|||||
Db 9 CTGCTAGAACTGCTAG 26

RESULT 9
CQ543182/c
LOCUS   CQ543182/c
DEFINITION Sequence 12817 from Patent WO0210449.
ACCESSION CQ543182
VERSION   CQ543182.1 GI:41509446
ORIGIN
Query Match 73.3%; Score 13.2; DB 6; Length 37;
Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCG 18
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Db 1 CTGCTAGAACTGCCCG 18
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KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 12817 07-FEB-2002;
Compugen Inc. (US)
FEATURES
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1. .60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 73.3%; Score 13.2; DB 6; Length 60;
Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CTGCTAGAACTGCCCG 18
Db 34 CTGCTTAGAACTGTTCTAG 17
RESULT 10
I32833/c
LOCUS I32833
DEFINITION Sequence 15 from patent US 5589364.
ACCESSION I32833
VERSION I32833.1 GI:1823624
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Williams,J.I., Pierce,J.C., Anderson,G.Mark. and Kari,P.
TITLE Recombinant production of biologically active peptides and proteins
JOURNAL Patent: US 5589364-A 15 31-DEC-1996;
FEATURES
source
1. .60
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 73.3%; Score 13.2; DB 6; Length 60;
Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CTGCTAGAACTGCCCG 18
Db 50 CTGCTTAAACTGCTAAG 33
RESULT 11
AX083959/c
LOCUS AX083959
DEFINITION Sequence 10 from Patent WO0112658.
ACCESSION AX083959
VERSION AX083959.1 GI:13185510
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Davis,S.
TITLE Human icos ligand and application thereof
JOURNAL Patent: WO 0112658-A 10 22-FEB-2001;
ISIS INNOVATION LIMITED (GB)
FEATURES
Location/Qualifiers
1. .65
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
us-10-655-801-20.max.rge
source
1. .62
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32830"
/note="Oligonucleotide"
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Query Match 73.3%; Score 13.2; DB 6; Length 62;
Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CTGCTAGAACTGCCCG 18
Db 62 CAGTCCAGGACTGCCCG 45
RESULT 12
CQ557381/c
LOCUS CQ557381
DEFINITION Sequence 27016 from Patent WO0210449.
ACCESSION CQ557381
VERSION CQ557381.1 GI:41523808
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 27016 07-FEB-2002;
Compugen Inc. (US)
FEATURES
source
1. .65
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
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Query Match 73.3%; Score 13.2; DB 6; Length 65;
Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CTGCTAGAACTGCCCG 18
Db 32 CTGCTCAGAAATGACCAG 15
RESULT 13
CQ559197
LOCUS CQ559197
DEFINITION Sequence 28832 from Patent WO0210449.
ACCESSION CQ559197
VERSION CQ559197.1 GI:41525624
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 28832 07-FEB-2002;
Compugen Inc. (US)
FEATURES
source
1. .65
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"
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ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 65;
Best Local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCAG 18
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Db 2 CTGTCAGAAATGCTCAG 19

RESULT 14

E14578
LOCUS DNA encoding repeat unit of artificial protein polymer. PAT 28-JUL-1999
DEFINITION E14578
ACCESSION E14578
VERSION E14578.1 GI:5709261
KEYWORDS JP 1997323999-A/3.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 70)
AUTHORS Fukushima, Y.
TITLE ARTIFICIAL PROTEIN POLYMER
JOURNAL Patent: JP 1997323999-A 3 16-DEC-1997;
UNITIKA LTD

COMMENT

OS None
OC Artificial sequences.
PN JP 1997323999-A/3
PD 16-DEC-1997
PF 03-JUN-1996 JP 1996139905
PI FUKUSHIMA YASUMASA
PC C07K14/435, C07H21/04, C12N1/21, (C12P21/02,
C12R1:19);
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..70
FT /organism='Artificial sequences'.
FT Location/Qualifiers

FEATURES

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ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTCTAGAACTGC 14
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Db 8 TGTCTAGAACTGC 20

RESULT 15

E14579/c
LOCUS DNA encoding repeat unit of artificial protein polymer. PAT 28-JUL-1999
DEFINITION E14579
ACCESSION E14579
VERSION E14579.1 GI:5709262
KEYWORDS JP 1997323999-A/4.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 70)
AUTHORS Fukushima, Y.
TITLE ARTIFICIAL PROTEIN POLYMER
JOURNAL Patent: JP 1997323999-A 4 16-DEC-1997;
UNITIKA LTD

COMMENT

OS None
OC Artificial sequences.

PN JP 1997323999-A/4
PD 16-DEC-1997
PF 03-JUN-1996 JP 1996139905
PI FUKUSHIMA YASUMASA
PC C07K14/435, C07H21/04, C12N1/21, (C12P21/02,
C12R1:19);
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..70
FT /organism='Artificial sequences'.
FT Location/Qualifiers

FEATURES

source
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ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGTCTAGAACTGC 14
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Db 67 TGTCTAGAACTGC 55

RESULT 16

AX273086
LOCUS Sequence 655 from Patent WO0162911. linear PAT 29-OCT-2001
DEFINITION AX273086
ACCESSION AX273086
VERSION AX273086.1 GI:16545823
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 655 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 71.1%; Score 12.8; DB 6; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGTCTAGAACTGCCCA 17
||||| ||||| ||||| |||||
Db 1 TGTCTGGAGCTGCCCA 16

RESULT 17

BD104284/c
LOCUS Kit and method for determining HLA type. linear PAT 27-AUG-2002
DEFINITION BD104284
ACCESSION BD104284
VERSION BD104284.1 GI:22649858
KEYWORDS WO 0192572-A/388.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)

AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.
 TITLE Kit and method for determining HLA type
 JOURNAL Patent: WO 0192572-A 389 06-DEC-2001;
 NISSHINBO INDUSTRIES INC.SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAeko
 KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
 NISHIDA
 COMMENT OS Artificial Sequence
 PN WO 0192572-A/389
 PD 06-DEC-2001
 PF 01-JUN-2001 WO 2001JP004662
 PR 01-JUN-2000 JP OOP 164798
 PI HIDETOSHI INOKO,TAeko KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI
 MATSUMURA,
 PC SHOGO MORIYA,MICHIO NISHIDA
 CC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
 Description of Artificial Sequence:capture
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 FT Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 ORIGIN
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 Best Local Similarity 87.5%; Pred.No.1.9e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CTGCTAGAACTGCC 16
 Db 18 CTGTCAGCACTGCC 3
 RESULT 18
 BD104285/c
 LOCUS BD104285 18 bp DNA linear PAT 27-AUG-2002
 DEFINITION Kit and method for determining HLA type.
 ACCESSION BD104285
 VERSION BD104285.1 GI:22649859
 KEYWORDS WO 0192572-A/389.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.
 TITLE Kit and method for determining HLA type
 JOURNAL Patent: WO 0192572-A 389 06-DEC-2001;
 NISSHINBO INDUSTRIES INC.SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAeko
 KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
 NISHIDA
 COMMENT OS Artificial Sequence
 PN WO 0192572-A/389
 PD 06-DEC-2001
 PF 01-JUN-2001 WO 2001JP004662
 PR 01-JUN-2000 JP OOP 164798
 PI HIDETOSHI INOKO,TAeko KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI
 MATSUMURA,
 PC SHOGO MORIYA,MICHIO NISHIDA
 CC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
 Description of Artificial Sequence:capture
 FH Key Location/Qualifiers
 FT source 1..18
 FT Location/Qualifiers
 1..18
 /organism="Artificial Sequence".
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 ORIGIN

Query Match 71.1%; Score 12.8; DB 6; Length 18;
 Best Local Similarity 87.5%; Pred.No.1.9e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CTGCTAGAACTGCC 16
 Db 18 CTGTCAGCACTGCC 3
 RESULT 19
 BD106033
 LOCUS BD106033 20 bp DNA linear PAT 18-SEP-2002
 DEFINITION Novel LDL-receptor.
 ACCESSION BD106033
 VERSION BD106033.1 GI:23200851
 KEYWORDS JP 2002501376-A/48.
 SOURCE Chlamydia sp.
 ORGANISM Chlamydia sp.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D., Hammond,H. and Hey,P.
 TITLE Novel LDL-receptor
 JOURNAL Patent: JP 2002501376-A 48 15-JAN-2002;
 THE WELLCOME TRUST LTD AS TRUSTEE TO THE WELLCOME TRUST, MERCK & CO
 INC
 COMMENT PN JP 2002501376-A/48
 PD 15-JAN-2002
 PF 15-APR-1998 JP 1998543635
 PR 15-APR-1997 US 60/043553,05-JUN-1997 US 60/048740 PI
 JOHN ANDREW TODD,JOHN WILFRED HESS,CHARLES
 THOMAS CASKEY,ROGER
 PI DAVID COX,
 PI DAVID GERHOLD,HOLLY HAMMOND,PATRICIA HEY
 PC C12N15/12,C12N15/11,C12Q1/68,C07K14/705,C07K16/28,A61K38/17,
 PC A61K39/395,
 PC A61K48/00
 CC Strandedness: Single;
 CC Topology: Linear;
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 /mol_type="genomic DNA"
 /db_xref="taxon:35827"
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 Best Local Similarity 87.5%; Pred.No.1.9e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 GTCTAGAACTGCCAG 18
 Db 4 GTCTGCACTGCCAG 19
 RESULT 20
 AR305122
 LOCUS AR305122 20 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 76 from patent US 6545137.
 ACCESSION AR305122
 VERSION AR305122.1 GI:31694432
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Todd,J.A., Hess,J.W., Caskey,C.T., Cox,R.D., Gerhold,D., Hammond,H., Hey,P., Kawaguchi,Y., Merriman,T.R., Metzker,M.L., Nakagawa,Y., Phillips,M.S. and Twells,R.C.J.
 TITLE Receptor
 JOURNAL Patent: US 6545137-A 76 08-APR-2003;

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  Best Local Similarity
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    14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY
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  ||||| ||||| |||||
Db
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RESULT 21
AR309226
LOCUS
  AR309226
  Sequence 76 from patent US 655654.
  linear PAT 12-JUN-2003
DEFINITION
  AR309226
ACCESSION
  AR309226
VERSION
  AR309226.1 GI:31701231
KEYWORDS
  Unknown.
SOURCE
  Unknown.
ORGANISM
  Unclassified.
  1 (bases 1 to 20)
  Todd, J.A., Hess, J.W., Caskey, C.T., Cox, R.D., Gerhold, D.,
  Hammond, H., Hey, P., Kawaguchi, Y., Merriman, T.R., Metzker, M.L.,
  Nakagawa, Y., Phillips, M.S. and Twells, R.C.J.
  LDL-receptor
  Patent: US 655654-A 76 29-APR-2003;
  The Wellcome Trust Limited as Trustee for the Wellcome Trust;
  London;
  WOX;
FEATURES
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Db
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RESULT 22
BD251172
LOCUS
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  Functional antagonists of hedgehog activity.
  linear PAT 17-JUL-2003
DEFINITION
  BD251172
ACCESSION
  BD251172
VERSION
  BD251172.1 GI:33060942
KEYWORDS
  JP 2002534060-A/3.
  Homo sapiens (human)
SOURCE
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominiidae; Homo.
  1 (bases 1 to 23)
  Williams, K., Rayhorn, P., Garber, E.A. and Pepinsky, B.R.
  Functional antagonists of hedgehog activity
  Patent: JP 2002534060-A 3 15-OCT-2002;
  BIOGEN INC
  OS Homo sapiens (human)
  PN JP 2002534060-A/3
  PD 15-OCT-2002
  PF 02-NOV-1999 JP 2000579170
  PR 02-NOV-1998 US 60/106703
  PI KEVIN WILLIAMS, PAUL RAYHORN, ELLEN A GARBER, BLAKE R PEPINSKY PC
  CL2N15/09, A61K38/00, A61P35/00, A61P43/00, C07K14/47, C07K17/08, PC

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C07K17/12,
PC
C07K19/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/00//C12Q1/ PC
42,
PC
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CC Functional antagonists of hedgehog activity
FH Key Location/Qualifiers
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Db
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RESULT 23
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LOCUS
  AX712114
  Sequence 27 from Patent WO03018798.
  linear PAT 11-APR-2003
DEFINITION
  AX712114
ACCESSION
  AX712114
VERSION
  AX712114.1 GI:29823355
KEYWORDS
  synthetic construct
  SOURCE
  synthetic construct
  other sequences; artificial sequences.
REFERENCE
  1
  AUTHORS
    Kaupmann, K.
  TITLE
    G-protein coupled receptor and dna sequences thereof
  JOURNAL
    Patent: WO 03018798-A 27 06-MAR-2003;
    Novartis AG (CH)
FEATURES
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  Matches
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QY
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  ||||| ||||| |||||
Db
  16 CTGTCTCGAAGCGCC 1
  ||||| ||||| |||||

RESULT 24
AR489327/c
LOCUS
  AR489327
  Sequence 80 from patent US 6709861.
  linear PAT 15-MAY-2004
DEFINITION
  AR489327
ACCESSION
  AR489327
VERSION
  AR489327.1 GI:47256285
KEYWORDS
  Unknown.
SOURCE
  Unknown.
ORGANISM
  Unclassified.
  1 (bases 1 to 38)
  Mead, D.A. and Godiska, R.
  Cloning vectors and vector components
  Patent: US 6709861-A 80 23-MAR-2004;
  Lucigen Corp.; Middleton, WI;
  WOX;

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source      Location/Qualifiers
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/organism="unknown"
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ORIGIN
Query Match      71.1%; Score 12.8; DB 6; Length 38;
Best Local Similarity 87.5%; Pred.No. 2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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    ||| |||||
Db 26 GTTACAACTGCCAG 11

RESULT 25
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LOCUS      51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 6582 from Patent WO0147944.
ACCESSION CQ007942
VERSION   CQ007942.1 GI:41014618
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini,
           Hominidae; Homo.
REFERENCE 1
AUTHORS   Shimkets, R.A. and Leach, M.
TITLE     Nucleic acids containing single nucleotide polymorphisms and
           methods of use thereof
JOURNAL   Patent: WO 0147944-A 6582 05-JUL-2001;
           Curagen Corporation (US)
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source      Location/Qualifiers
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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    ||| |||||
Db 33 CTGTCCAGAACAGCCC 48

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Job time : 377.932 secs

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OM nucleic - nucleic search, using sw model

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Title: US-10-655-801-20

Perfect score: 18
Sequence: 1 ctgcttagaactgcccag 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 5180220

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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9: Geneseqn2003bs:*
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13: Geneseqn2004bs:*
14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	100.0	18	AAH47976	AAH47976 Human ind
2	15.4	85.6	22	AD113013	AD113013 PCR prime
3	14.8	82.2	76	ABN51490	ABN51490 Human cDN
4	13.8	76.7	65	ABN54635	ABN54635 Mouse spl
5	13.4	74.4	20	AAH97601	AAH97601 Murine SA
6	13.4	74.4	20	ADMI5941	ADMI5941 Murine SA
7	13.4	74.4	30	AAH43849	AAH43849 Human HAH
8	13.4	74.4	60	ABN44109	ABN44109 Human spl
9	13.2	73.3	20	ADN58822	ADN58822 Human B7H
10	13.2	73.3	25	AAH88302	AAH88302 Human CD3
11	13.2	73.3	25	ACI78021	ACI78021 Human mic
12	13.2	73.3	37	ABN52868	ABN52868 Plasmid p
13	13.2	73.3	50	ABZ04767	ABZ04767 Human leu
14	13.2	73.3	50	ADP10075	ADP10075 50-mer ol
15	13.2	73.3	60	ABN35482	ABN35482 Human spl
16	13.2	73.3	60	ABN40059	ABN40059 Human spl
17	13.2	73.3	62	AAH00425	AAH00425 Human B7-
18	13.2	73.3	65	ABN56084	ABN56084 Mouse spl
19	13.2	73.3	65	ABN54268	ABN54268 Mouse spl

79	10	ACD93864	73.3	13.2	20	ACD93864	Human col
30	12	ADQ77297	72.2	13	21	ADQ77297	Chicken m
35	4	AAF57115	72.2	13	22	AAF57115	NtCBP4 co
17	4	ABL47022	71.1	12.8	23	ABL47022	Human GRI
17	11	ADM54345	71.1	12.8	24	ADM54345	Human GRI
17	14	ABE23669	71.1	12.8	25	ABE23669	HLA-DP al
18	6	ABL30899	71.1	12.8	26	ABL30899	Human HLA
18	6	ABL30900	71.1	12.8	27	ABL30900	Human HLA
20	2	AAV85580	71.1	12.8	28	AAV85580	LRP5 PCR
22	14	ADZ03943	71.1	12.8	29	ADZ03943	Myocardia
23	3	AAA28858	71.1	12.8	30	AAA28858	Primer 1
25	9	ACI67516	71.1	12.8	31	ACI67516	Human mic
25	9	ACH57974	71.1	12.8	32	ACH57974	DNA carge
28	8	ABZ79479	71.1	12.8	33	ABZ79479	Nested ge
38	6	ABQ75054	71.1	12.8	34	ABQ75054	Bacteriop
51	4	AAL33374	71.1	12.8	35	AAL33374	Human SNP
51	4	AAH40224	71.1	12.8	36	AAH40224	Human SNP
54	13	ADM50708	71.1	12.8	37	ADM50708	PCR prime
60	6	ABN39580	71.1	12.8	38	ABN39580	Human spl
60	6	ABN47630	71.1	12.8	39	ABN47630	Human spl
60	6	ABN44906	71.1	12.8	40	ABN44906	Human spl
15	6	ABN54060	68.9	12.4	41	ABN54060	Human mon
18	11	ADZ43420	68.9	12.4	42	ADZ43420	PCR prime
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27	2	AAQ38725	68.9	12.4	44	AAQ38725	AVP probe
27	12	ADM13058	68.9	12.4	45	ADM13058	Recombina
29	13	ADT66489	68.9	12.4	46	ADT66489	PCR prime
39	12	ADK41336	68.9	12.4	47	ADK41336	Human chr
41	2	AAV50754	68.9	12.4	48	AAV50754	Brassica
51	4	AAL28476	68.9	12.4	49	AAL28476	Human SNP
57	3	AAZ24684	68.9	12.4	50	AAZ24684	Oligonuc
57	3	AAZ96685	68.9	12.4	51	AAZ96685	T cell an
67	2	AAH36295	68.9	12.4	52	AAH36295	Human col
72	2	AAQ44684	68.9	12.4	53	AAQ44684	8F10-stim
72	2	AAH84404	67.8	12.2	54	AAH84404	STM7.1 ge
21	2	AAH85563	67.8	12.2	55	AAH85563	PCR prime
22	13	ADT00687	67.8	12.2	56	ADT00687	Novel mut
25	9	ACK19326	67.8	12.2	57	ACK19326	Human mic
25	9	ACI70251	67.8	12.2	58	ACI70251	Human mic
27	3	AAH70510	67.8	12.2	59	AAH70510	Novel hum
27	4	AAH78477	67.8	12.2	60	AAH78477	Nucleotid
27	8	ACC49274	67.8	12.2	61	ACC49274	Human RFR
29	3	AAZ35698	67.8	12.2	62	AAZ35698	Mouse imm
30	6	ABX68776	67.8	12.2	63	ABX68776	Novel Hel
30	14	ADN00258	67.8	12.2	64	ADN00258	PCR prime
32	12	ADN97350	67.8	12.2	65	ADN97350	PCR prime
40	11	ADM96528	67.8	12.2	66	ADM96528	Oligonuc
50	5	ABA13725	67.8	12.2	67	ABA13725	Human ner
50	6	ABZ06809	67.8	12.2	68	ABZ06809	Human leu
50	6	ABN33115	67.8	12.2	69	ABN33115	Human leu
60	6	ABN59517	67.8	12.2	70	ABN59517	Human spl
60	6	ABN46001	67.8	12.2	71	ABN46001	Human spl
60	6	ABN44981	67.8	12.2	72	ABN44981	Human spl
62	4	AAF70940	67.8	12.2	73	AAF70940	BEGF DNA
62	2	AAAT00354	67.8	12.2	74	AAAT00354	Family 3
65	6	ABN54413	67.8	12.2	75	ABN54413	Mouse spl
65	6	ABN29081	67.8	12.2	76	ABN29081	Rat splic
65	6	ABN53253	67.8	12.2	77	ABN53253	Mouse spl
22	2	ADT95476	66.7	12	78	ADT95476	Primer fo
22	12	ADL46145	66.7	12	79	ADL46145	HIV-1 gag
22	12	ADL46143	66.7	12	80	ADL46143	VSV G gly
25	9	ACH63932	66.7	12	81	ACH63932	DNA targ
30	2	AAH75519	66.7	12	82	AAH75519	3' primer
30	6	ABK27410	66.7	12	83	ABK27410	Human pap
30	6	ABK27409	66.7	12	84	ABK27409	Human pap
40	2	AAQ35140	66.7	12	85	AAQ35140	PCR prime
40	2	AAV09373	66.7	12	86	AAV09373	Rev and e
60	6	ABN36305	66.7	12	87	ABN36305	Human spl
60	6	ABN34729	66.7	12	88	ABN34729	Human spl
65	6	ABZ29819	65.6	11.8	89	ABZ29819	Candida g
17	2	AAH71000	65.6	11.8	90	AAH71000	Human KDR
17	4	ABL47263	65.6	11.8	91	ABL47263	Human GRI
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93 11.8 65.6 17 11 ADM54583
 C 94 11.8 65.6 17 14 AEB23697
 C 95 11.8 65.6 20 12 ADM58929
 96 11.8 65.6 20 12 ADM58772 Human B7H
 97 11.8 65.6 20 12 ADQ74729
 98 11.8 65.6 20 13 ADS19750
 C 99 11.8 65.6 20 13 ADS19683 Human PTP
 100 11.8 65.6 20 14 ADW44854 Human tax

ALIGNMENTS

RESULT 1
 AAH47976
 ID AAH47976 standard; DNA; 18 BP.
 XX
 AC AAH47976;
 XX
 XX 02-OCT-2001 (first entry)
 XX
 XX Human inducible NOS antisense oligonucleotide SEQ ID NO 20.
 DE
 XX Antisense oligonucleotide; inducible nitric oxide synthase; NOS;
 KW modulate expression; immunomodulator; antidiabetic; cardiovascular;
 KW cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;
 KW 2'-O-methoxyethyl; phosphorothioate; human; ss.
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH modified_base 1..18
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone, 5' and 3' four
 FT nucleotide 2'-MOE (2'-O-methoxyethyl) wings (the cytidine
 FT residues in the 2'-MOE wings are 5-methylcytidines) and a
 FT deoxy gap"
 FT
 PN W0200152902-Al.
 XX
 XX 26-JUL-2001.
 XX
 XX 15-JAN-2001; 2001WO-US001381.
 XX
 XX 24-JAN-2000; 2000US-00490208.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Bennett CF, Dean NM, Cowser LM;
 PI
 XX WPI; 2001-465340/50.
 DR
 XX
 XX New antisense oligonucleotides for modulating the expression of inducible
 PT nitric oxide synthase in cells or tissues, particularly useful for
 PT treating e.g. immunological, cardiovascular or neurological disorders, or
 PT ischemia.
 PS
 XX Claim 3; Page 83; 144pp; English.
 XX
 XX The invention relates to antisense compounds, especially
 CC oligonucleotides, which are targeted to a nucleic acid encoding inducible
 CC nitric oxide synthase and which specifically hybridize to and modulate
 CC expression of inducible nitric oxide synthase. The antisense compounds
 CC have immunomodulator, antidiabetic, cardiovascular, cardiant,
 CC neuroprotective, disorder and vasotropic activity. The antisense
 CC oligonucleotides are useful for inhibiting the expression of inducible
 CC nitric oxide synthase in cells or tissues. In particular, the antisense
 CC oligonucleotides are useful for treating diseases or disorders associated
 CC with inducible nitric oxide synthase, e.g. diabetes, immunological
 CC disorder, cardiovascular disorder, neurological disorder or
 CC ischaemia/reperfusion injury. The antisense oligonucleotides are also
 CC useful for research and diagnostics. The present sequence is that of an

CC antisense 2'-O-methoxyethyl gapmer oligonucleotide with a
 CC phosphorothioate backbone, a central "gap" region of ten nucleotides
 CC flanked by four nucleotide 2'-MOE (2'-methoxyethyl) wings (cytidine
 CC residues in the 2'-MOE wings are 5-methylcytidines) and targeted to human
 CC inducible nitric oxide synthase (NOS) mRNA (AAH47959)
 XX
 SQ Sequence 18 BP; 4 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCCAG 18
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 Db 1 CTGCTAGAACTGCCCAG 18

RESULT 2

AD113013
 ID AD113013 standard; DNA; 22 BP.
 XX
 AC AD113013;
 XX
 XX 22-APR-2004 (first entry)
 XX
 DE PCR primer used to amplify human NOR-1 (MINOR) DNA SeqID 7.
 XX
 KW human; PCR; ss; allergic disease; NOR-1; MINOR; eosinophil;
 KW atopic dermatitis; anti-allergic; anti-inflammatory; dermatological;
 KW primer.
 XX Homo sapiens.
 XX
 XX WO2004003198-Al.
 PN
 XX 08-JAN-2004.
 XX
 XX 27-JUN-2003; 2003WO-JP008199.
 PF
 XX 27-JUN-2002; 2002JP-00189490.
 PR
 XX (GENO-) GENOX RES INC.
 XX (NIGE-) JAPAN GEN AGENCY NATION.
 PA
 XX Hashida R, Kagaya S, Yayoi Y, Sugita Y, Saito H;
 PI
 XX WPI; 2004-083057/08.
 DR
 XX Examining allergic diseases e.g. atopic dermatitis by differential
 PT display based on gene expression of NOR-1 receptor protein, also
 PT applicable in screening compounds for treatment of allergic diseases.
 XX
 XX Example 1; SEQ ID NO 7; 155pp; Japanese.
 PS
 XX This invention relates to a novel method for examining allergic diseases
 CC that comprises comparing the expression levels of a gene encoding the NOR
 CC -1 receptor protein between patients and healthy individuals.
 CC Specifically, the NOR-1 gene, also referred to as MINOR, is expressed in
 CC the specialist white blood cells known as eosinophils and is involved in
 CC mediating an allergic reaction. The present invention describes a
 CC differential display method that can identify the expression level of
 CC this gene in order to identify its usefulness in diagnosing allergic
 CC diseases such as atopic dermatitis. Furthermore, compositions can also be
 CC used to screen compounds for the treatment of allergic diseases.
 CC Accordingly, they exhibit various activities including anti-allergic,
 CC anti-inflammatory and dermatological. This oligonucleotide sequence is a
 CC PCR primer used to amplify human NOR-1 DNA in an exemplification of the
 CC invention.
 XX
 SQ Sequence 22 BP; 5 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 12; Length 22;
 Best Local Similarity 94.1%; Pred. No. 2.4e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCTAGAACTGCCAG 18
Db 6 TGCTAGAACTGCCAG 22

RESULT 3

ABNS51490
ID ABS51490 standard; cDNA; 76 BP.

XX AC
XX AC
XX ABS51490;

XX 21-OCT-2002 (first entry)

XX Human cDNA encoding prey protein for Shigella ospC1 #15.

XX ss; gene; prey protein; ospB; ospD1; ipaD; ipaC; ipaH9.8; ospG; ospC1;
KW Shigella; shigellosis; bacillary dysentery; antibacterial;
KW yeast two-hybrid system; protein-protein interaction; SID;
KW selected interacting domain; human.

XX Homo sapiens.

XX WO200257303-A2.

XX 25-JUL-2002.

XX 11-JAN-2002; 2002WO-EP000777.

XX 12-JAN-2001; 2001US-0261130P.

XX (HYBR-) HYBRIGENICS.

XX Legrain P;

XX WPI; 2002-599706/64.

XX P-PSDB; ABG70097.

XX New complex of protein-protein interactions between a bait Shigella
PT flexneri polypeptide and a prey mammalian or human placenta polypeptide
PT for treating or preventing bacillary dysentery in a mammal or human.

PS Claim 8; Page 79; 162pp; English.

XX The invention relates to a complex of protein-protein interactions
CC between a Shigella flexneri polypeptide (e.g. ospB, ospD1, ipaD, ipaC,
CC ipaH9.8, ospG and ospC1) and a mammalian polypeptide defined in the
CC specification. The complexes are formed using the yeast two-hybrid
CC system. Also included are (1) a recombinant host cell expressing the
CC interactions between the Shigella flexneri polypeptide and a mammalian
CC polypeptide defined in the specification; (2) selecting a modulating
CC compound that inhibits or activates the protein-protein interactions; (3)
CC a modulating compound obtained from the method of (2); (4) a SID
CC (selected interacting domain) polypeptide or its fragment or variant
CC comprising the human polypeptides appearing as ABG70042-ABG70242; (5) a
CC SID polynucleotide or its fragment or variant comprising encoding the
CC above polypeptides a vector comprising (5); (6) a recombinant host cell
CC containing the vector; and (10) a protein chip comprising Shigella
CC flexneri polypeptide and a mammalian polypeptide defined in the
CC specification. A pharmaceutical composition comprising the compound,
CC polypeptide or polynucleotide is useful for treating or preventing
CC shigellosis (bacillary dysentery) in a human or mammal. The present
CC sequence encodes a human prey protein isolated by the yeast two-hybrid
CC assay, forming a complex of the invention with a shigella protein

XX SQ Sequence 76 BP; 18 A; 19 C; 20 G; 19 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 6; Length 76;

Best Local Similarity 88.9%; Pred. No. 5.9e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCAG 18

Db 20 CTTCTAGAAATGCCAG 37

RESULT 4

ABNS54635

ID ABNS54635 standard; DNA; 65 BP.

XX AC

XX ABNS54635;

XX 15-JUL-2002 (first entry)

XX Mouse spliced transcript detection oligonucleotide SEQ ID NO:27383.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;

XX splice variant; transcriptome; oligonucleotide library; ss.

XX Mus musculus.

XX WO200210449-A2.

XX 07-FEB-2002.

XX 20-JUL-2001; 2001WO-IB001903.

XX 28-JUL-2000; 2000US-0221607P.

XX 02-MAY-2001; 2001US-0287724P.

XX (COMP-) COMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX WPI; 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which

XX selectively hybridize to mRNAs transcribed from a transcription unit of a

XX genome, useful for detecting tissue-, pathology-, and developmental-

XX specific genes.

XX Example 1; SEQ ID NO 27383; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting

XX messenger RNAs that populate a (sub-)transcriptome, where the (sub-

XX)transcriptome comprises messenger RNAs transcribed from multiple

XX transcription units that populate a genome. The library comprises several

XX oligonucleotides, each capable of hybridising selectively to a set of

XX messenger RNAs transcribed from a given transcription unit of the genome,

XX which encodes one or more messenger RNA splice variants. The

XX oligonucleotide libraries are useful for detecting mRNAs from a

XX biological sample, in expression profiling studies, in qualitatively or

XX quantitatively characterising the corresponding transcriptome, and in

XX detecting RNA transcripts and splice variants of human or animal

XX transcriptomes. The libraries may also be used as specialised mini

XX libraries to detect transcripts of a sub-transcriptome under a particular

XX biological or pathological state, and so allowing the detection of tissue

XX - and pathology-specific genes such as those genes only expressed in

XX specific tissue under a specific pathological condition; to detect

XX developmental specific genes; and to detect RNA transcripts and splice

XX variants of a transcriptome of a patient suffering from a particular

XX disorder. ABN27253 to ABNS5989 represent oligonucleotide sequences from

XX rats, humans and mice, which are used in the exemplification of the

XX present invention. N.B. The sequence data for this patent did not form

XX part of the printed specification, but was obtained in electronic format

XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 65 BP; 9 A; 16 C; 17 G; 23 T; 0 U; 0 Other;

Query Match 76.7%; Score 13.8; DB 6; Length 65;

Best Local Similarity 88.2%; Pred. No. 2e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCAG 17

```

Db      18 CTGCTTGTGCACTGCCA 34

RESULT 5
AAS97601
ID      AAS97601 standard; DNA; 20 BP.
XX
AC      AAS97601;
XX
DT      12-MAR-2002 (first entry)
XX
DE      Murine SAC1 gene-specific oligonucleotide PCR primer #206.
XX
KW      Human; mouse; SAC1; carbohydrate; sweetener; ethanol; alcoholism; ss;
KW      obesity; diabetes; transgenic embryo; body tissue; body fluid; pancreas;
KW      blood; tongue; PCR primer; anorectic; antidiabetic; gene therapy;
KW      protein replacement therapy.
XX
OS      Mus sp.
XX
PN      W0200183749-A2.
XX
PD      08-NOV-2001.
XX
PF      25-APR-2001; 2001WO-US013387.
XX
PR      28-APR-2000; 2000US-0200794P.
PR      28-JUL-2000; 2000US-0221419P.
PR      10-NOV-2000; 2000US-0247443P.
XX
PA      (WARN ) WARNER LAMBERT CO.
PA      (MONE-) MONELL CHEM SENSES CENT.
XX
PI      Bachmanov AA, Beauchamp GK, Chatterjee A, De Jong PJ, Li S, Li X;
PI      Ohmen JD, Reed DR, Ross D, Tordoff MG;
XX
WPI; 2002-075162/10.
XX
Novel isolated polypeptide comprising variant form of mouse or human SAC1
PT polypeptide, and is associated with altered preference for carbohydrates
PT or other sweeteners, useful for preventing obesity, diabetes, alcoholism.
XX
PS      Claim 14; Page 81; 239pp; English.
XX
The invention relates to an isolated polypeptide, comprising a variant
CC form of mouse or human SAC1 polypeptide. The variant form is associated
CC with altered preference for carbohydrates, other sweeteners or ethanol.
CC The polypeptide and its associated DNA sequence can be produced by
CC recombinant techniques and is useful for preventing obesity, diabetes or
CC alcoholism associated with SAC1 expression. The sequences are useful in
CC screening for drugs and sweeteners. Recombinant cell lines and transgenic
CC embryos may be used in screening for and identifying agents that induce
CC or repress function of SAC1. Predisposition to diabetes, obesity or
CC alcoholism can be ascertained by testing any fluid or tissue of a human
CC (such as blood, pancreas or tongue) for sequence variations of the SAC1
CC gene. A sequence variation of the SAC1 locus may indicate a
CC predisposition to diabetes, obesity and/or alcoholism and may provide a
CC diagnostic mark. The polynucleotide can be detected in a biological
CC sample by contacting the DNA with a probe to form a hybridisation complex
CC which is then detected. The sequences represent cDNA encoding human and
CC mouse SAC1 polypeptides and PCR primers specific for the SAC1 genes
XX
SQ      Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;
Query Match          74.4%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1 CTGCTTAGAAGTGC 15
         |||||
Db      4 CTGCTTAGAAGTGC 18

```

```

RESULT 6
ADM15941
ID      ADM15941 standard; DNA; 20 BP.
XX
AC      ADM15941;
XX
DT      15-JUL-2004 (first entry)
XX
DE      Murine SAC1 DNA PCR primer #206.
XX
KW      Mouse; SAC1; PCR; ss; carbohydrate; sweetener; ethanol; obesity;
KW      diabetes; alcoholism; antidiabetic; alcohol; anorectic; antialcoholic;
KW      primer.
XX
OS      Mus musculus.
XX
PN      US2004081964-A1.
XX
PD      29-APR-2004.
XX
PF      25-OCT-2002; 2002US-00280183.
XX
PR      25-OCT-2002; 2002US-00280183.
XX
PA      (BACH/) BACHMANOV A A.
PA      (BEAU/) BEAUCHAMP G K.
PA      (LISS/) LI S.
PA      (LIXX/) LI X.
PA      (REED/) REED D R.
PA      (TORD/) TORDOFF M G.
PA      (ROSS/) ROSS D A.
PA      (OHMA/) OHMAN J D.
PA      (CHAT/) CHATTERJEE A.
PA      (DJON/) DE JONG P J.
XX
PI      Bachmanov AA, Beauchamp GK, Li S, Li X, Reed DR, Tordoff MG;
PI      Ross DA, Ohman JD, Chatterjee A, De Jong PJ;
XX
WPI; 2004-340133/31.
XX
New isolated polynucleotides for sensing carbohydrates, other sweeteners,
PT or ethanol, useful for screening drugs for inhibition or restoration of
PT gene function as antidiabetic, antiobesity or antialcohol consumption
PT therapies.
XX
Example 12; SEQ ID NO 211; 148pp; English.
XX
The invention relates to SAC1 polypeptides and the polynucleotides
CC encoding them. The polynucleotides contain a variation associated with
CC sensing carbohydrates, other sweeteners or ethanol. The invention also
CC relates to a method for analysing a biomolecule in a biological sample,
CC comprising altering SAC1 activity in the sample and measuring the
CC activity, a method for analysing a polynucleotide in a biological sample,
CC comprising contacting a polynucleotide in a biological sample with a
CC probe where the probe hybridises to a SAC1 polynucleotide to form a
CC hybridisation complex and detecting the hybridisation complex, a method
CC of identifying susceptibility to obesity or diabetes comprising comparing
CC the nucleotide sequence of the suspected SAC1 allele with a wild type
CC nucleotide sequence, where the difference between the suspected allele
CC and the wild-type sequence identifies a sequence variation of the SAC1
CC nucleotide sequence, and a method of treating or preventing obesity,
CC diabetes or alcoholism associated with expression of SAC1, comprising
CC administering to a subject a pharmaceutical composition and a transgenic
CC animal that carries an altered SAC1 allele. The methods and compositions
CC of the invention are useful for screening drugs for inhibition or
CC restoration of gene function as antidiabetic, antiobesity or antialcohol
CC consumption therapies and for identifying sweeteners and alcohols. This
CC sequence represents a PCR primer used to amplify murine SAC1 DNA of the
CC invention.
XX
SQ      Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;
Query Match          74.4%; Score 13.4; DB 12; Length 20;

```


Best Local Similarity 93.3%; Pred. No. 3e+03; Mismatches 0; Gaps 0; Indels 1; Length 30;

Qy 1 CTGTCTAGAACTGCC 15
| | | | | | | | | |
Db 4 CTGTCTAGAACTGCC 18

RESULT 7

AA43849
ID AAD43849 standard; DNA; 30 BP.

XX
AC AAD43849;
XX

XX
DT 14-NOV-2002 (first entry)
XX

XX
DE Human HAH1 DNA amplifying PCR primer #2.
XX

XX
KW Single stranded polynucleotide tag; cleavage agent; gene expression;
KW human; PCR; primer; ss.
XX

XX
OS Homo sapiens.
XX

XX
PN WO200259357-A2.
XX

XX
PD 01-AUG-2002.
XX

XX
PF 24-JAN-2002; 2002WO-DK000052.
XX

XX
PR 24-JAN-2001; 2001DK-00000126.
XX

XX
PR 12-FEB-2001; 2001US-0267704P.
XX

XX
PA (GENO-) GENOMIC EXPRESSION APS.
XX

XX
PI Pedersen ML;
XX

XX
DR WPI; 2002-636542/68.
XX

XX
PT Obtaining single stranded polynucleotide tags from a biological sample,
PT for analyzing gene expression or diagnosing clinical conditions,
PT comprises employing nicking endonucleases that cleave complementary
PT strands.
XX

XX
PS Example; Page 293; 302pp; English.
XX

XX
CC The invention relates to a method for obtaining a single stranded
CC polynucleotide tag from a biological sample by cleaving one of the
CC complementary strands of a double stranded polynucleotide with a cleavage
CC agent capable of recognising a double stranded polynucleotide comprising
CC complementary strands and cleaving only one of the strands of the
CC polynucleotide in the process of generating a single stranded
CC polynucleotide tag. The method is useful for separating, analysing,
CC quantifying or obtaining single stranded polynucleotides comprising tags
CC originating partly, and preferably wholly from a source of DNA and/or RNA
CC in a sample comprising biological cells. The method is particularly for
CC analysing gene expression (expression profiling or differential gene
CC expression), or in diagnosing clinical conditions. The present sequence
CC is human HAH1 DNA amplifying PCR primer. This sequence is used in the
CC exemplification of the invention
XX

SQ Sequence 30 BP; 6 A; 10 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 74.4%; Score 13.4; DB 6; Length 30;
Best Local Similarity 93.3%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTAGAACTGCCAG 18
| | | | | | | | | |
Db 3 TCTAGAACTGCCAG-17

RESULT 8

ABN44109/c

ID ABN44109 standard; DNA; 60 BP.

XX
AC ABN44109;
XX

XX
DT 15-JUL-2002 (first entry)
XX

XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:16857.
XX

XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX

XX
OS Homo sapiens.
XX

XX
PN WO200210449-A2.
XX

XX
PD 07-FEB-2002.
XX

XX
PF 20-JUL-2001; 2001WO-IB001903.
XX

XX
PR 28-JUL-2000; 2000US-0221607P.
XX

XX
PR 02-MAY-2001; 2001US-0287724P.
XX

XX
PA (COMP-) COMPUGEN INC.
XX

XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX

XX
DR WPI; 2002-257383/30.
XX

XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX

XX
PS Example 1; SEQ ID NO 16857; 47pp; English.
XX

XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 60 BP; 20 A; 15 C; 14 G; 11 T; 0 U; 0 Other;

Query Match 74.4%; Score 13.4; DB 6; Length 60;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTAGAACTGCCAG 18
| | | | | | | | | |
Db 16 TCTAGAACTGCCAG 2

RESULT 9

ADN58822

ID ADN58822 standard; DNA; 20 BP.

```

XX AC ADN58822;
XX AC
XX DT 12-AUG-2004 (first entry)
XX DE Human B7H antisense oligonucleotide ISIS 205933.
XX KW B7H; autoimmune disease; ss; antisense; human.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN US2004102398-A1.
XX XX
XX PD 27-MAY-2004.
XX XX
XX PF 23-NOV-2002; 2002US-00303420.
XX XX
XX PR 23-NOV-2002; 2002US-00303420.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX XX
XX PI Monia BP, Dobie KW;
XX XX
XX DR WPI; 2004-399728/37.
XX XX
XX PT New compound targeted to a nucleic acid molecule encoding B7H and
XX FT inhibits expression of B7H, useful for modulating the expression of B7H
XX PT or for diagnosing or treating, e.g. autoimmune disease.
XX XX
XX PS Example 15; SEQ ID NO 73; 97pp; English.
XX XX
XX CC The invention relates to a compound targeted to a nucleic acid molecule
XX CC encoding B7H, where the compound specifically hybridises with the nucleic
XX CC acid molecule encoding B7H and inhibits the expression of B7H. The
XX CC compound is useful for modulating the expression of B7H. It is also
XX CC useful for diagnosing or treating diseases associated with expression of
XX CC B7H, e.g. an autoimmune disease. The present sequence represents a human
XX CC B7H antisense oligonucleotide.
XX XX
XX SQ Sequence 20 BP; 4 A; 9 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 12; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGTCTAGAACTGCCCG 18
   |||||
Db 1 CAGTCCAGGACTGCCCG 18

RESULT 10
AA88302
ID AAX88302 standard; DNA; 24 BP.
XX AC
XX AC AAX88302;
XX XX
XX DT 28-SEP-1999 (first entry)
XX XX
XX DE Human CD30 antigen binding domain PCR primer 1.
XX XX
XX KW CD30; antigen binding domain; human; suppressor; cell proliferation;
XX KW tumour formation; metastasis; CD30-antigen expressing cell; antisense;
XX KW cellular activation; cell death; cell lysis; anticancer; treatment;
XX KW CD30-expressing tumour; amplification; PCR primer; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX XX
XX PN DE1988967-A1.
XX XX
XX PD 12-AUG-1999.
XX XX

PF 06-FEB-1998; 98DE-01038967.
XX PR
XX XX 06-FEB-1998; 98DE-01038967.
XX PA (ABKE/) ABKEN H.
XX PI Abken H;
XX XX
XX DR WPI; 1999-445521/38.
XX XX
XX PT Suppressing proliferation, tumor formation and metastasis of CD30-
XX PT positive cells by contact with specific binding agent, for treating
XX PT tumors.
XX XX
XX PS Example 3; Page 3; 8pp; German.
XX XX
XX CC This invention describes a novel method for the suppression of unlimited
XX CC proliferation, tumour formation and metastasis of CD30-antigen expressing
XX CC cells and uses a molecule (I) that binds specifically to CD30 without
XX CC causing cellular activation through CD30. (I) inhibit cell proliferation
XX CC by an antisense mechanism or, where (I) is an antibody, by induction of
XX CC cell death/lysis. CD30+ L540 lymphoma cells (104 ml-1) were incubated
XX CC with 10 mu g/ml of single-chain Fv anti-CD30 polypeptide, and after 6
XX CC days metabolism of tetrazolium salt to formazan measured to estimate cell
XX CC viability. (I) have anticancer activity and are used to treat CD30-
XX CC expressing tumours. This sequence represents a PCR primer used to amplify
XX CC the human CD30 antigen binding domain
XX XX
XX SQ Sequence 24 BP; 5 A; 8 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 2; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGTCTAGAACTGCCCG 18
   |||||
Db 7 CAGTCTAGAACTGCCCG 24

RESULT 11
AC178021
ID AC178021 standard; DNA; 25 BP.
XX AC
XX AC AC178021;
XX XX
XX DT 14-OCT-2003 (first entry)
XX XX
XX DE Human microarray DNA oligonucleotide SEQ ID NO 78012.
XX XX
XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX KW genetic variation; biallelic marker; polymorphism; human;
XX KW cross-species comparison.
XX OS Homo sapiens.
XX XX
XX PN US2003104410-A1.
XX XX
XX PD 05-JUN-2003.
XX XX
XX PF 15-MAR-2002; 2002US-00098263.
XX XX
XX PR 16-MAR-2001; 2001US-0276759P.
XX XX
XX PA (AFFY-) AFFYMETRIX INC.
XX XX
XX PI Mittmann MP;
XX XX
XX DR WPI; 2003-567953/53.
XX XX
XX PT New array of nucleic acid probes, useful for in situ hybridization, in
XX PT Southern, Northern or dot-blot hybridization to identify or detect the
XX PT sequence or specific mutations of any gene.
XX XX

```

PS Claim 1; SEQ ID NO 78012; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

CC Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in *in situ* hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

XX

XX Sequence 25 BP; 6 A; 7 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTCTAGAACTGCCACG 18
||| ||||| ||| |||

Db 8 CTCTCTAGAACTGCCAAG 25

RESULT 12

ABS52868

ID ABS52868 standard; DNA; 37 BP.

AC ABS52868;

XX

XX 27-NOV-2002 (first entry)

DE Plasmid pML-Ptac PCR primer #5.

XX

XX Expression control sequence; microbiology; operon leader; PCR; primer; bacterial gene expression; p-independent transcription terminator; pML-Ptac; ss.

OS Synthetic.

XX

XX EP1234893-A1.

PN

XX

XX 28-AUG-2002.

PD

XX

XX 30-JAN-2002; 2002EP-00002298.

PF

XX

XX 22-FEB-2001; 2001RU-00104817.

PR

XX

XX (AJIN) AJINOMOTO CO INC.

PA

XX

XX Mashko SV, Zimenkov DV;

PI

XX

XX WPI; 2002-659523/71.

DR

XX

XX An expression control sequence which controls expression of a target gene linked downstream of the expression control sequence depending on an intracellular concentration of an amino.

PT

XX

XX Example 1; Page 11; 32pp; English.

PS

XX

CC The invention relates to an expression control sequence which controls expression of a target gene linked downstream of the expression control sequence depending on an intracellular concentration of an amino acid. In the bacterium which harbours a DNA construct containing the expression control sequence, a promoter linked upstream and the target gene linked downstream of the expression control sequence, the frequency of termination of transcription is lowered by increase of an intracellular concentration of an amino acid whereby expression of the target gene increases. The expression sequence is useful for the microbiological industry in particular to the development of a new approach to the regulated gene expression in bacterial cells. The present sequence represents a PCR primer used to construct the plasmid pML-Ptac

XX

XX Sequence 37 BP; 11 A; 11 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 6; Length 37;
Best Local Similarity 83.3%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTCTAGAACTGCCACG 18
||| ||||| ||| |||

Db 4 CTGCTCTAGAACTGCCAAG 21

RESULT 13

ABZ04767

ID ABZ04767 standard; DNA; 50 BP.

XX

XX ABZ04767;

AC

XX

XX 09-JAN-2003 (first entry)

DT

XX

XX Human leukocyte gene expression profiling probe SEQ ID NO 4758.

DE

XX

XX T7; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe; ss.

KW

XX

XX Homo sapiens.

OS

XX

XX WO200257414-A2.

PN

XX

XX 25-JUL-2002.

PD

XX

XX 22-OCT-2001; 2001WO-US047856.

PF

XX

XX 20-OCT-2000; 2000US-0241994P.

PR

XX

XX 08-JUN-2001; 2001US-0296764P.

PR

XX

XX (BIOC-) BIOCARDIA INC.

PA

XX

XX Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J; Ly N, Woodward R, Quettermous T, Johnson F;

PI

XX

XX WPI; 2002-636525/68.

DR

XX

XX New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.

PT

XX

XX Claim 1; Page 480; Opp; English.

PS

XX

XX The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection,

CC

CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ Sequence 50 BP; 18 A; 17 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 6; Length 50;
Best Local Similarity 83.3%; Pred. No. 4.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCAG 18
Db 17 CAGACTACAACTGCCAG 34

RESULT 14
ADP10075
ID ADP10075 standard; DNA; 50 BP.
XX
AC ADP10075;
XX
DT 12-AUG-2004 (first entry)
XX
DE 50-mer oligonucleotide marker probe of the invention #84.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
XX
OS Homo sapiens.
XX
FN WO2004042346-A2.
XX
PD 21-MAY-2004.
XX
PF 24-APR-2003; 2003WO-US012946.
XX
PR 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M,
PI Rosenberg S;
XX
WPI; 2004-400724/37.
XX
PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
PS Claim 2; SEQ ID NO 84; 1762pp; English.
XX
CC The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing and monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC 50 mer oligonucleotide marker for diagnosis and monitoring of allograft
CC rejection and other disorders.
XX
SQ Sequence 50 BP; 18 A; 17 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 12; Length 50;
Best Local Similarity 83.3%; Pred. No. 4.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCAG 18
Db 17 CAGACTACAACTGCCAG 34

RESULT 15
ABN35482
ID ABN35482 standard; DNA; 60 BP.
XX
AC ABN35482;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:8230.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
PS Example 1; SEQ ID NO 8230; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 60 BP; 12 A; 15 C; 18 G; 15 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 6; Length 60;
Best Local Similarity 83.3%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCAG 18

Db 9 CTGTCAGACTGCCTAG 26
|||||

RESULT 16
ABN40069/c
ID ABN40069 standard; DNA; 60 BP.

XX AC ABN40069;

XX DT 15-JUL-2002 (first entry)

XX DE Human spliced transcript detection oligonucleotide SEQ ID NO:12817.

XX KW Human; mouse; rat; splice transcript; detection; RNA transcript;

XX KW splice variant; transcriptome; oligonucleotide library; ss.

XX OS Homo sapiens.

XX PN WO200210449-A2.

XX PD 07-FEB-2002.

XX PF 20-JUL-2001; 2001WO-IB001903.

XX PR 28-JUL-2000; 2000US-0221607P.

XX PR 02-MAY-2001; 2001US-0287724P.

XX PA (COMP-) COMPUGEN INC.

XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX DR WPI; 2002-257383/30.

XX PT New oligonucleotide libraries comprising oligonucleotides which

PT selectively hybridize to mRNAs transcribed from a transcription unit of a

PT genome, useful for detecting tissue-, pathology-, and developmental-

XX specific genes.

PS Example 1; SEQ ID NO 12817; 47pp; English.

CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 60 BP; 20 A; 13 C; 12 G; 15 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 6; Length 60;

Best Local Similarity 83.3%; Pred. No. 4.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGTCAGACTGCCTAG 18

|||||

Db 34 CTGCTTGAAGTGTTCAG 17

RESULT 17

AAS00425/c

ID AAS00425 standard; DNA; 62 BP.

XX AC AAS00425;

XX DT 11-MAY-2001 (first entry)

XX DE Human B7-3 5'-RT PCR primer.

XX KW Human; B7-3; inducible co-stimulator; ICOS; TU-D; KIAA0653; CD28; T-cell;
XX ICOS-mediated activity; IL-10 production; TH2 activity;

XX KW Helicobacter pylori induced peptic ulcer; Crohn's disease;

XX KW multiple sclerosis; type I diabetes mellitus; graft rejection;

XX KW helminth infection; allergic disease; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200112658-A2.

XX PD 22-FEB-2001.

XX PF 10-AUG-2000; 2000WO-GB003079.

XX PR 11-AUG-1999; 99US-0148402P.

XX PA (ISIS-) ISIS INNOVATIONS LTD.

XX PI Davis S;

XX DR WPI; 2001-226547/23.

XX PT New B7-3 polypeptides useful for modulating inducible co-stimulator
PT protein and for treating ulcers, Crohn's disease, multiple sclerosis,
PT diabetes mellitus, infections and allergic diseases.

PS Disclosure; Page 62; 77pp; English.

CC The present sequence for B7-3 5'-RT PCR primer is used with B7-3 3'-RT
CC PCR primer (AAS00426) to amplify human B-cell RNA to isolate a novel B7-3
CC protein which acts as a ligand for inducible co-stimulator (ICOS)
CC protein. The B7-3 protein previously referred to as TU-D or KIAA0653 was
CC considered by the 2 groups as being incomplete. The present inventor has
CC determined the sequence to be complete and renamed the sequence as B7-3.
CC Also described is a soluble form of B7-3 (AAU00423) which comprises the
CC B7-3 signal sequence and extracellular domain. The extracellular domain
CC is shown to bind ICOS which is related to CD28 and expressed on T-cells.
CC B7-3 polypeptides or its fragments are useful for identifying a substance
CC which interacts with the polypeptide or its fragment. B7-3 polypeptides,
CC fragments, tetramer, an agent with an ability to affect B7-3 activity or
CC a specific binding member are useful for modulating an ICOS-mediated
CC activity of T-cells by modulating IL-10 production and TH2 activity, and
CC for manufacturing a medicament for modulating an ICOS-mediated activity
CC of T-cells. B7-3 polypeptides are useful for development of diagnostic,
CC prophylactic and therapeutic agents for diseases such as Helicobacter
CC pylori induced peptic ulcers, Crohn's disease, multiple sclerosis, type I
CC diabetes mellitus, graft rejection, helminth infections, and allergic
CC diseases

XX SQ Sequence 62 BP; 13 A; 20 C; 17 G; 12 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 4; Length 62;

Best Local Similarity 83.3%; Pred. No. 4.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTGAAGTGTTCAG 18

|||||

Db 62 CAGTCCAGGACTGCCAG 45

```
RESULT 18
ABN56084
ID ABN56084 standard; DNA; 65 BP.
XX
AC ABN56084,
XX
DT 15-JUL-2002 (first entry)
XX
DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:28832.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Mus musculus.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
PS Example 1; SEQ ID NO 28832; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-)
CC transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 65 BP; 15 A; 16 C; 16 G; 18 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 6; Length 65;
Best Local Similarity 83.3%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCAG 18
| | | | | | | | | | | | | | | |
Dd 2 CTGTCCAGAAATGCTCAG 19
| | | | | | | | | | | | | | | |

RESULT 19
ABN54268/c
ID ABN54268 standard; DNA; 65 BP.
XX
AC ABN54268;
XX
DT 15-JUL-2002 (first entry)
XX
DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:27016.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Mus musculus.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
PS Example 1; SEQ ID NO 27016; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-)
CC transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 65 BP; 13 A; 19 C; 13 G; 20 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 6; Length 65;
Best Local Similarity 83.3%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCAG 18
| | | | | | | | | | | | | | | |
Dd 32 CTGTCCAGAAATGACCAG 15
| | | | | | | | | | | | | | | |

RESULT 20
ACD93864
```

```

ID ACD93864 standard; cDNA; 79 BP.
XX
AC ACD93864;
XX
XX
DT 23-SEP-2003 (first entry)
XX
DE Human colon cancer cell expressed cDNA #2276.
XX
XX Open reading frame detection; genome sequencing; colon cancer;
KW breast cancer; population genome analysis; genetic shift; cancer;
KW antibiotic resistance; antibiotic non-tolerance; congenital disease;
KW agriculture; food crop genome; resistance gene; retrovirus;
KW influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
KW gene; ss.
XX
XX Homo sapiens.
XX
XX US2002155438-A1.
XX
XX 24-OCT-2002.
XX
XX 27-SEP-1999; 99US-00406117.
XX
XX 20-NOV-1998; 98US-00196716.
XX
XX (SIMP/) SIMPSON A J G.
PA (NETO/) NETO E D.
PA (BREN/) BRENTANI R R.
XX
XX Simpson AJG, Neto ED, Brentani RR;
XX
XX WPI; 2003-182626/18.
DR
XX
PT Determining open reading frames of genome of an organism e.g. a human
PT suffering from cancer involves use of single oligonucleotide primer at
PT low stringency for preparing single-stranded cDNA from mRNA of
PT individual.
XX
XX Example 9; Page 347-348; 959pp; English.
XX
XX The invention describes a method of determining open reading frames in
CC the genome of organism, comprising contacting mRNA from cell of organism
CC with a single oligonucleotide primer (I) at low stringency, preparing
CC single-stranded cDNA by reverse transcribing mRNA with (I), amplifying
CC cDNA, sequencing the product, and repeating the contacting, preparing
CC and amplifying steps with different primers and sequencing resulting
CC nucleic acids. The method is useful for: determining that a known
CC nucleotide sequence from a genome of an organism corresponds to a
CC nucleotide sequence of an open reading frame; for preparing a contig,
CC nucleic acid molecule from a genome of an organism; and for sequencing
CC all or part of a genome of an organism. mRNA is obtained from mammalian
CC or human cell which is associated with a pathological condition e.g. a
CC colon cancer or breast cancer cell. The method is useful for analyses of
CC populations of subjects and can be used to carry out genetic analyses of
CC large or small populations. Further, it can be used to study living
CC systems to determine if, e.g. there have been genetic shifts which render
CC an individual or population more or less likely to be afflicted with
CC diseases such as cancer, to determine antibiotic resistance or non-
CC tolerance, and so forth. The method can also be used in the study of
CC congenital diseases, and the risk of affliction to a foetus, as well as
CC the study of whether the conditions are likely to be passed to offspring
CC through ova or sperm. The analyses for pathological conditions can be
CC carried out in all animals, plants, birds, fish, etc. Using this method,
CC in the area of agriculture, for example the genomes of food crops can be
CC studied to determine if resistance genes are present, defects in plant
CC genomes can also be studied in this way. Similarly, the method permits
CC determination of the pathogens which integrate into the genome, such as
CC retroviruses and other integrating viruses such as influenza virus, have
CC undergone shifts or mutations, which may require different approaches to
CC therapy. This method is also applied to eukaryotic pathogens, such as
CC trypanosomes, different types of Plasmodium, etc. The method essentially
CC eliminates sequencing of non-coding portions. This sequence represents a
CC polynucleotide isolated from human colon cancer cell cDNA library

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XX
SQ Sequence 79 BP; 15 A; 32 C; 18 G; 14 T; 0 U; 0 Other;
Query Match 73.3%; Score 13.2; DB 10; Length 79;
Best Local Similarity 83.3%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CTGCTAGAACTGCCCG 18
DB 16 CTGCCAGAACTCCCG 33
||| ||| ||| ||| ||| ||| |||
RESULT 21
ADQ77297
ID ADQ77297 standard; DNA; 30 BP.
XX
XX AC ADQ77297;
XX
XX DT 07-OCT-2004 (first entry)
XX
XX DE Chicken matrix associated region (MAR) PCR primer, SEQ ID NO:2.
XX homologous recombination; somatic cell; DT40 cell; chicken;
KW matrix associated region; MAR; PCR; primer; ss.
XX
XX Gallus gallus.
XX
XX WO2004058964-A1.
XX
XX 15-JUL-2004.
XX
XX 22-DEC-2003; 2003WO-JP016496.
XX
XX 26-DEC-2002; 2002JP-00376555.
XX
XX (RIKE) RIKEN KK.
PA (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.
XX
XX Ohta K, Seo H, Shibata T;
XX
XX WPI; 2004-525881/50.
XX
XX Inducing DNA homologous recombination in somatic cell useful for
PT acquiring novel genes, involves regulating transcription of gene in
PT arbitrary locus and inducing recombination between gene and another gene
PT having similar sequence.
XX
XX Example 1; SEQ ID NO 2; 37pp; Japanese.
XX
XX The specification describes a method for inducing homologous DNA
CC recombination in somatic cells, e.g. DT40 cells. The method involves
CC regulating transcriptional activity of a gene existing on an arbitrary
CC locus in the cell and thus inducing homologous DNA recombination between
CC the gene and another gene having a similar sequence. The method is useful
CC for isolating novel genes with plural genetic data. It enables
CC spontaneous acquisition of objective genes with genetic diversity,
CC without a library preparation step. PCR primers ADQ77296-ADQ77297 were
CC used to amplify a chicken matrix associated region (MAR), for use in the
CC method of the invention.
XX
XX Sequence 30 BP; 9 A; 10 C; 3 G; 8 T; 0 U; 0 Other;
Query Match 72.2%; Score 13; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TCTAGAACTGCC 16
DB 3 TCTAGAACTGCC 15
||| ||| ||| ||| ||| ||| |||
RESULT 22
AAF57115/c

```


PT New nucleic acid molecule that down-regulates expression of Grb2-related
PT with insert domain (GRID) gene, useful for treating a condition
PT associated with the level of GRID, e.g. tissue/graft rejection and
PT leukemia.

XX Claim 4; SEQ ID NO 655; 74pp; English.

XX The invention relates to a nucleic acid molecule that down-regulates
CC expression of Grb2-related with insert domain (GRID) gene, e.g. a
CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyme, DNase, a
CC amberyzyme, inozyme or hairpin ribozyme. Also include are a mammalian cell
CC including the novel nucleic acid molecule, reducing GRID activity in a
CC cell by contacting the cell with the novel nucleic acid molecule,
CC treating a patient having a condition associated with the level of GRID
CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
CC contacting the cell with the novel nucleic acid molecule, an expression
CC vector comprising a nucleic acid sequences (encoding at least the novel
CC nucleic acid molecule in a manner that allows its expression), a
CC mammalian cell including the expression vector and an enzymatic nucleic
CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
CC molecule is useful for treating a condition associated with the level of
CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
CC a target region for the enzymatic nucleic acids of the invention.

XX SQ Sequence 17 BP; 2 A; 6 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 11; Length 17;

Best Local Similarity 62.5%; Pred. No. 6.2e+03;

Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCTCTAGAACTGCCCA 17

Db 1 UGUCUGGAGCGGCCA 16

RESULT 25

AEB23669/c

ID AEB23669 standard; DNA; 17 BP.

AC AEB23669;

XX 22-SEP-2005 (first entry)

DE HLA-DP allele identification-related oligonucleotide probe SeqID212.

KW HLA-DP; human leukocyte antigen; diagnostic; SNP detection;

KW DNA detection; Transplant rejection; cancer; diabetes; probe; ss.

OS Homo sapiens.

XX JP2005185175-A.

PN 14-JUL-2005.

XX 25-DEC-2003; 2003JP-00430557.

PR 25-DEC-2003; 2003JP-00430557.

XX (CANO) CANON KK.

PA Tsukada M;

XX WPI; 2005-515774/53.

XX Probe set for identifying human leukocyte antigen (HLA)-DP allele in test
PT substance in patients with organ transplant, cancer, diabetes, comprises
PT probes such as DPA1.010301, DPA1.010302, DPA1.0104, DPA1.0105,
PT DPB1.010101, or DPB1.010102.

PS Claim 2; SEQ ID NO 212; 32pp; Japanese.

XX This invention relates to a novel probe set for identifying HLA-DP (human

CC leukocyte antigen-DP) alleles in a test substance. The invention enables
CC identification of HLA-DP alleles in patients with organ transplant,
CC cancer, diabetes and other multiple-factor diseases, and thus provides
CC tailored medical treatment to individual patients. The present sequence
CC is that of an oligonucleotide probe which is used in the HLA-DP probe set
CC of the present invention.

XX SQ Sequence 17 BP; 3 A; 5 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 14; Length 17;

Best Local Similarity 87.5%; Pred. No. 6.2e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCC 16

Db 17 CTGTCCGGAAGTCCC 2

Search completed: March 3, 2006, 08:00:27

Job time : 124.534 secs

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 OM nucleic - nucleic search, using sw model
 Run on: March 3, 2006, 07:29:32 ; Search time 23.6441 Seconds
 (without alignments)
 1353.240 Million cell updates/sec

Title: US-10-655-801-20
 Perfect score: 18
 Sequence: 1 ctgtctagaactgcccag 18
 Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1395746

Minimum DB seq length: 0
 Maximum DB seq length: 80

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

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 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:
 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:
 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:
 5: /cgn2_6/ptodata/1/ina/H COMB.seq:
 6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:
 7: /cgn2_6/ptodata/1/ina/FP COMB.seq:
 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:
 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	13.4	74.4	25	3	US-09-396-196G-5801
C 2	13.4	74.4	25	3	US-09-396-196G-5802
C 3	13.4	74.4	30	3	US-10-053-883-49
C 4	13.2	73.3	25	3	US-09-396-196G-29403
C 5	13.2	73.3	25	3	US-09-396-196G-29404
C 6	13.2	73.3	25	3	US-09-396-196G-113025
C 7	13.2	73.3	50	3	US-10-131-827-4758
C 8	13.2	73.3	53	6	PCT-US95-10219-13
C 9	13.2	73.3	53	6	PCT-US95-10219-13
C 10	13.2	73.3	60	2	US-08-282-030-15
C 11	13.2	73.3	60	6	PCT-US95-10219-15
C 12	12.8	71.1	20	3	US-09-060-299-76
C 13	12.8	71.1	20	3	US-09-402-923A-76
C 14	12.8	71.1	25	3	US-09-396-196G-24036
C 15	12.8	71.1	25	3	US-09-396-196G-86286
C 16	12.8	71.1	25	3	US-09-396-196G-108974
C 17	12.8	71.1	38	3	US-10-001-052-80
C 18	12.4	68.9	25	3	US-09-396-196G-5723
C 19	12.4	68.9	25	3	US-09-396-196G-5724
C 20	12.4	68.9	25	3	US-09-396-196G-12464
C 21	12.4	68.9	25	3	US-09-396-196G-12465
C 22	12.4	68.9	47	3	US-09-422-978-410
C 23	12.2	67.8	25	3	US-09-098-628-64
C 24	12.2	67.8	25	3	US-09-396-196G-5483

C 25	12.2	67.8	25	3	US-09-396-196G-5484	Sequence 5484, Ap
C 26	12.2	67.8	25	3	US-09-396-196G-41203	Sequence 41203, A
C 27	12.2	67.8	25	3	US-09-396-196G-52243	Sequence 52243, A
C 28	12.2	67.8	25	3	US-09-396-196G-97883	Sequence 97883, A
C 29	12.2	67.8	25	3	US-09-396-196G-97884	Sequence 97884, A
C 30	12.2	67.8	25	3	US-09-396-196G-124884	Sequence 124884, A
C 31	12.2	67.8	25	3	US-09-673-245-1	Sequence 1, Appl
C 32	12.2	67.8	25	3	US-10-131-827-6410	Sequence 6410, Ap
C 33	12.2	67.8	50	3	US-10-131-827-6800	Sequence 6800, Ap
C 34	12.2	67.8	62	3	US-08-687-421-402	Sequence 402, App
C 35	12	66.7	22	2	US-08-639-501-92	Sequence 92, Appl
C 36	12	66.7	22	2	US-09-044-948-92	Sequence 92, Appl
C 37	12	66.7	22	3	US-09-044-908-92	Sequence 92, Appl
C 38	12	66.7	30	2	US-08-458-120-4	Sequence 4, Appl
C 39	12	66.7	30	2	US-08-867-970-4	Sequence 4, Appl
C 40	12	66.7	30	3	US-09-326-217-4	Sequence 4, Appl
C 41	12	66.7	30	3	US-09-732-020-4	Sequence 4, Appl
C 42	12	66.7	30	3	US-09-876-258-10	Sequence 10, Appl
C 43	12	66.7	30	3	US-09-876-258-11	Sequence 11, Appl
C 44	12	66.7	40	2	US-08-147-890-10	Sequence 10, Appl
C 45	11.8	65.6	16	3	US-09-371-772B-6968	Sequence 6968, Ap
C 46	11.8	65.6	17	3	US-08-584-040-3750	Sequence 3750, Ap
C 47	11.8	65.6	17	3	US-09-371-772B-1517	Sequence 1517, Ap
C 48	11.8	65.6	17	3	US-09-371-772B-6132	Sequence 6132, Ap
C 49	11.8	65.6	17	3	US-09-685-664B-1517	Sequence 1517, Ap
C 50	11.8	65.6	25	3	US-09-396-196G-19933	Sequence 19933, A
C 51	11.8	65.6	25	3	US-09-396-196G-9380	Sequence 9380, Ap
C 52	11.8	65.6	25	3	US-09-396-196G-19934	Sequence 19934, A
C 53	11.8	65.6	25	3	US-09-396-196G-19935	Sequence 19935, A
C 54	11.8	65.6	25	3	US-09-396-196G-96302	Sequence 96302, A
C 55	11.8	65.6	25	3	US-09-396-196G-96303	Sequence 96303, A
C 56	11.8	65.6	25	3	US-09-396-196G-103286	Sequence 103286, A
C 57	11.8	65.6	25	3	US-09-396-196G-103287	Sequence 103287, A
C 58	11.8	65.6	25	3	US-09-396-196G-103288	Sequence 103288, A
C 59	11.8	65.6	25	3	US-09-396-196G-123769	Sequence 123769, A
C 60	11.8	65.6	27	3	US-09-023-045-8	Sequence 8, Appl
C 61	11.8	65.6	27	3	US-09-435-321-8	Sequence 8, Appl
C 62	11.8	65.6	28	3	US-09-940-244-237	Sequence 297, App
C 63	11.8	65.6	28	3	US-09-777-430C-33	Sequence 33, Appl
C 64	11.8	65.6	30	2	US-08-276-852-28	Sequence 28, Appl
C 65	11.8	65.6	30	2	US-08-133-011-35	Sequence 35, Appl
C 66	11.8	65.6	30	2	US-08-437-815-7	Sequence 7, Appl
C 67	11.8	65.6	30	2	US-08-322-730A-35	Sequence 35, Appl
C 68	11.8	65.6	30	2	US-08-162-102C-16	Sequence 16, Appl
C 69	11.8	65.6	30	2	US-08-387-874-35	Sequence 35, Appl
C 70	11.8	65.6	30	2	US-08-899-575-28	Sequence 28, Appl
C 71	11.8	65.6	30	2	US-08-899-575-28	Sequence 28, Appl
C 72	11.8	65.6	30	2	US-08-897-040-7	Sequence 7, Appl
C 73	11.8	65.6	30	2	US-08-383-619-35	Sequence 35, Appl
C 74	11.8	65.6	30	3	US-08-907-739-35	Sequence 35, Appl
C 75	11.8	65.6	30	3	US-08-972-564-14	Sequence 14, Appl
C 76	11.8	65.6	30	3	US-09-386-642-56	Sequence 56, Appl
C 77	11.8	65.6	30	3	US-09-723-597-35	Sequence 35, Appl
C 78	11.8	65.6	30	3	US-08-920-100B-16	Sequence 16, Appl
C 79	11.8	65.6	30	6	PCT-US93-08364-35	Sequence 35, Appl
C 80	11.8	65.6	30	6	PCT-US93-08786-16	Sequence 16, Appl
C 81	11.8	65.6	30	6	PCT-US95-00667-16	Sequence 16, Appl
C 82	11.8	65.6	30	6	PCT-US95-08743-28	Sequence 28, Appl
C 83	11.8	65.6	34	3	US-09-481-620A-98	Sequence 98, Appl
C 84	11.8	65.6	42	3	US-09-139-802-213	Sequence 213, App
C 85	11.8	65.6	42	3	US-09-139-802-214	Sequence 214, App
C 86	11.8	65.6	42	3	US-09-139-802-215	Sequence 215, App
C 87	11.8	65.6	42	3	US-09-659-786-213	Sequence 213, App
C 88	11.8	65.6	42	3	US-09-659-786-214	Sequence 214, App
C 89	11.8	65.6	42	3	US-09-659-786-215	Sequence 215, App
C 90	11.8	65.6	42	3	US-09-889-480A-15	Sequence 15, Appl
C 91	11.8	65.6	44	3	US-09-139-802-216	Sequence 216, App
C 92	11.8	65.6	44	3	US-09-659-786-216	Sequence 216, App
C 93	11.8	65.6	47	9	5217864-5	Patent No. 5217864
C 94	11.8	65.6	50	3	US-10-131-827-6174	Sequence 6174, Ap
C 95	11.8	65.6	51	3	US-08-676-818-24	Sequence 24, Appl
C 96	11.8	65.6	51	3	US-09-407-549-24	Sequence 24, Appl
C 97	11.8	65.6	51	3	US-09-407-728-24	Sequence 24, Appl

c 98 11.8 65.6 65 2 US-08-468-012A-4
c 99 11.8 65.6 65 3 US-09-054-989-4
c 100 11.8 65.6 65 3 US-09-662-746A-4

Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-396-196G-5801/c
; Sequence 5801, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5801
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-5801

Query Match 74.4%; Score 13.4; DB 3; Length 25;
Best Local Similarity 93.3%; Pred. No. 5.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCC 15
Db 21 CTGCTAGAACTGCC 7

RESULT 2

US-09-396-196G-5802/c
; Sequence 5802, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5802
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-5802

Query Match 74.4%; Score 13.4; DB 3; Length 25;
Best Local Similarity 93.3%; Pred. No. 5.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCC 15
Db 15 CTGCTAGAACTGCC 1

RESULT 3

US-10-053-883-49
; Sequence 49, Application US/10053883
; Patent No. 6958217
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Morten Lorentz
; TITLE OF INVENTION: ASSAY AND KIT FOR ANALYZING GENE EXPRESSION
; FILE REFERENCE: PEDERSEN=1A
; CURRENT APPLICATION NUMBER: US/10/053,883
; CURRENT FILING DATE: 2002-01-02
; PRIOR FILING DATE: 2001-01-24
; PRIOR FILING DATE: 2001-01-24
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-053-883-49

Query Match 74.4%; Score 13.4; DB 3; Length 30;
Best Local Similarity 93.3%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCTAGAACTGCCACG 18
Db 3 TCTAGAACTGCCAAG 17

RESULT 4

US-09-396-196G-29403/c
; Sequence 29403, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29403
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-29403

Query Match 73.3%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCACG 18
Db 25 CTGCTAGAACTGCCACG 8

RESULT 5

US-09-396-196G-29404/c
; Sequence 29404, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.

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; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29404
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-29404

Query Match      73.3%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCCCG 18
Db 23 CTGTCTAGAACTGCCCG 6

RESULT 6
US-09-396-196G-113025/c
; Sequence 113025, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113025
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-113025

Query Match      73.3%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCCCG 18
Db 21 CTGTCTAGAACTGCCCG 4

RESULT 7
US-10-131-827-4758
; Sequence 4758, Application US/10111827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08

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; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4758
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-4758

Query Match      73.3%; Score 13.2; DB 3; Length 50;
Best Local Similarity 83.3%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCCCG 18
Db 17 CAGACTCAACTGCCCG 34

RESULT 8
US-08-282-030-13
; Sequence 13, Application US/08282030
; Patent No. 5589364
; GENERAL INFORMATION:
; APPLICANT: Williams, Jon I.
; APPLICANT: Pierce, James C.
; APPLICANT: Anderson, Mark G.
; APPLICANT: Kari, Prasad
; TITLE OF INVENTION: Recombinant Production of Biologically
; TITLE OF INVENTION: Active Peptides and Proteins
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,030
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fordis, Jean B.
; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 05387.0001-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-282-030-13

Query Match      73.3%; Score 13.2; DB 2; Length 53;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCCCG 18
Db 15 CTGTCTAGAACTGCCCG 32

RESULT 9
PCT-US95-10219-13
; Sequence 13, Application PC/TUS9510219

```

GENERAL INFORMATION:
APPLICANT: Williams, Jon I.
APPLICANT: Pierce, James C.
APPLICANT: Anderson, Mark G.
APPLICANT: Karl, Prasad
TITLE OF INVENTION: Recombinant Production of Biologically
TITLE OF INVENTION: Active Peptides and Proteins
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10219
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,030
FILING DATE: 29-JUL-1994
NAME: Fordis, Jean B.
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0001-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-10219-13

Query Match 73.3%; Score 13.2; DB 6; Length 53;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCAG 18
|||||
Db 15 CTGCTAAACTGCTAAG 32

RESULT 10
US-08-282-030-15/c
Sequence 15, Application US/08282030
Patent No. 5589364
GENERAL INFORMATION:
APPLICANT: Williams, Jon I.
APPLICANT: Pierce, James C.
APPLICANT: Anderson, Mark G.
APPLICANT: Karl, Prasad
TITLE OF INVENTION: Recombinant Production of Biologically
TITLE OF INVENTION: Active Peptides and Proteins
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,030
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0001-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-282-030-15

Query Match 73.3%; Score 13.2; DB 2; Length 60;
Best Local Similarity 83.3%; Pred. No. 7.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCAG 18
|||||
Db 50 CTGCTAAACTGCTAAG 33

RESULT 11
PCT-US95-10219-15/c
Sequence 15, Application PC/TUS9510219
GENERAL INFORMATION:
APPLICANT: Williams, Jon I.
APPLICANT: Pierce, James C.
APPLICANT: Anderson, Mark G.
APPLICANT: Karl, Prasad
TITLE OF INVENTION: Recombinant Production of Biologically
TITLE OF INVENTION: Active Peptides and Proteins
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10219
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,030
FILING DATE: 29-JUL-1994
NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0001-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-10219-15

Query Match 73.3%; Score 13.2; DB 6; Length 60;
Best Local Similarity 83.3%; Pred. No. 7.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCAG 18
||||| ||||| ||
Db 50 CTGCTAAACTGCTAG 33

RESULT 12

US-09-060-299-76
Sequence 76, Application US/09060299
Patent No. 6545137

GENERAL INFORMATION:

APPLICANT: Todd, John A
APPLICANT: Hess, John W
APPLICANT: Caskey, Charles T
APPLICANT: Cox, Roger D
APPLICANT: Gerhold, David
APPLICANT: Hammond, Holly
APPLICANT: Hey, Patricia
APPLICANT: Kawaguchi, Yoshihiko
APPLICANT: Merriman, Tony R
APPLICANT: Metzker, Michael L
TITLE OF INVENTION: No. 6545137el Receptor
NUMBER OF SEQUENCES: 455
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon and Vanderhye
STREET: 1100 No. 6545137th Glebe Road, Eighth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: US

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,299
FILING DATE: 15-APR-1998
CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US 60/043,553
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/048,740
FILING DATE: 05-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: B.J.Sadoff
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-35

TELEPHONE: (703)816-4091
TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-060-299-76

Query Match 71.1%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GTCTAGAACTGCCAG 18
||||| ||||| |||||

RESULT 14

US-09-396-196G-24036
Sequence 24036, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann

QY 3 GTCTAGAACTGCCAG 18
||||| ||||| |||||

Db 4 GTCTGAACTTCCAG 19

RESULT 13

US-09-402-923A-76
Sequence 76, Application US/09402923A
Patent No. 655654

GENERAL INFORMATION:

APPLICANT: Todd, John A
APPLICANT: Hess, John W
APPLICANT: Caskey, Charles T
APPLICANT: Cox, Roger D
APPLICANT: Gerhold, David
APPLICANT: Hammond, Holly
APPLICANT: Hey, Patricia
APPLICANT: Kawaguchi, Yoshihiko
APPLICANT: Merriman, Tony R
APPLICANT: Metzker, Michael L
TITLE OF INVENTION: No. 655654el LDL-Receptor
NUMBER OF SEQUENCES: 455
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon and Vanderhye
STREET: 1100 No. 655654th Glebe Road, Eighth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: US
ZIP: VA 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,923A
FILING DATE: 14-Feb-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01102
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/043,553
FILING DATE: 15-APR-1997

APPLICATION NUMBER: US 60/048,740
FILING DATE: 05-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: B.J.Sadoff
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 620-81

TELEPHONE: (703)816-4091
TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-402-923A-76

Query Match 71.1%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GTCTAGAACTGCCAG 18
||||| ||||| |||||

Db 4 GTCTGAACTTCCAG 19

```

; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24036
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-24036

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Query Match          71.1%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 3 GTCTAGAACTGCCCAG 18
Db 6 GTCCAGAGCTGCCCAG 21

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RESULT 15
US-09-396-196G-86286
; Sequence 86286, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396.196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86286
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-86286

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Query Match      71.1%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 CTGTCTAGAACTGCC 16
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Dp 10 CTGTCTAGAGCTGGCC 25
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RESULT 16
US-09-396-196G,108974
/ Sequence 108974, Application US/09396196G
/ Patent No. 6821724
/ GENERAL INFORMATION:
/ APPLICANT: Michael Mittmann
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/09/396,196G
/ CURRENT FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17

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; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 108974
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-108974

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Query Match 71.1%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. NO. 1.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 3 GTCTAGAACTGCCCAG 18
Db 5 GTCCAGAACTACCCAG 20

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RESULT 17
US-10-001-052-80/c
; Sequence 80, Application US/10001052
; Patent No. 6709861
; GENERAL INFORMATION:
; APPLICANT: Mead, David A.
; APPLICANT: Godiska, Ronald
; TITLE OF INVENTION: CLONING VECTORS AND VECTOR COMPONENTS
; FILE REFERENCE: MICRO-06635
; CURRENT APPLICATION NUMBER: US/10/001,052
; CURRENT FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 80
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-001-052-80

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Query Match      71.1%; Score 12.8; DB 3; Length 38;
Best Local Similarity 87.5%; Pred. No. 1.2e+03;
Matches 14: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 3 GTCTAGAACTGCCCAG 18
Db 26 GTTTACAACCTGCCCAG 11

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RESULT 18
US-09-396-196G-5723
; Sequence 5723, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5723
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-5723

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Query Match 68.9%; Score 12.4; DB 3; Length 25;
Best Local Similarity 92.9%; Pred. No. 2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels

Qy 5 CTAGAACTGCCAG 18
Db 8 CTAAGAACTGCCAG 21

RESULT 19

US-09-396-196G-5724
; Sequence 5724, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; PRIOR FILING DATE: 1999-09-15

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 5724

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-396-196G-5724

Query Match 68.9%; Score 12.4; DB 3; Length 25;

Best Local Similarity 92.9%; Pred. No. 2e+03; Indels 1; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Gaps 0;

Qy 5 CTAGAACTGCCAG 18
Db 2 CTAAGAACTGCCAG 15

RESULT 20

US-09-396-196G-12464

; Sequence 12464, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; PRIOR FILING DATE: 1999-09-15

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 12464

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-396-196G-12464

Query Match 68.9%; Score 12.4; DB 3; Length 25;

Best Local Similarity 92.9%; Pred. No. 2e+03; Indels 1; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Gaps 0;

Qy 4 TCTAGAACTGCCCA 17
Db 8 TCCAGAACTGCCCA 21

RESULT 21

US-09-396-196G-12465

; Sequence 12465, Application US/09396196G

; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12465
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-12465

Query Match 68.9%; Score 12.4; DB 3; Length 25;

Best Local Similarity 92.9%; Pred. No. 2e+03; Indels 1; Gaps 0;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTAGAACTGCCCA 17
Db 2 TCCAGAACTGCCCA 15

RESULT 22

US-09-422-978-410

; Sequence 410, Application US/09422978

; Patent No. 6537751

; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta

; APPLICANT: Chumakov, Ilya

; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

; FILE REFERENCE: GENSET.020CPI

; CURRENT APPLICATION NUMBER: US/09/422,978

; PRIOR FILING DATE: 1999-10-20

; PRIOR FILING DATE: 1999-04-21

; EARLIER APPLICATION NUMBER: US 09/298,850

; EARLIER APPLICATION NUMBER: US 60/109,732

; EARLIER APPLICATION NUMBER: US 60/082,614

; EARLIER APPLICATION NUMBER: US 60/082,614

; NUMBER OF SEQ ID NOS: 11796

; SEQ ID NO 410

; LENGTH: 47

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: allele

; LOCATION: 24

; OTHER INFORMATION: 99-1469-47 : polymorphic base G or C

US-09-422-978-410

Query Match 68.9%; Score 12.4; DB 3; Length 47;

Best Local Similarity 81.2%; Pred. No. 2.1e+03;

Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCC 16
Db 11 CTGCCTAGAACTGSAC 26

RESULT 23

US-09-098-628-64

; Sequence 64, Application US/09098628

; Patent No. 6294359

; GENERAL INFORMATION:

; APPLICANT: FIDDES, J.C.

; APPLICANT: ABRAHAM, J.D.
; TITLE OF INVENTION: HUMAN BASIC FIBROBLAST GROWTH
; TITLE OF INVENTION: FACTOR ANALOG
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,628
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 21900-20089.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-098-628-64

Query Match 67.8%; Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCCA 17
||| ||| ||| ||| |||
Db 9 CTGCTGGAAGTGGCA 25

RESULT 24
US-09-396-196G-5483/c
; Sequence 5483, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5483
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-5483

Query Match 67.8%; Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.5e+03;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CTGCTAGAACTGCCCA 17
||| ||| ||| ||| |||
Db 24 CTTCTGGGACTGCCCA 8
RESULT 25
US-09-396-196G-5484/c
; Sequence 5484, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5484
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-5484

Query Match 67.8%; Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCCA 17
||| ||| ||| ||| |||
Db 23 CTTCTGGGACTGCCCA 7

Search completed: March 3, 2006, 07:34:53
Job time : 24.6441 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:34:36 ; Search time 221.11 Seconds
(without alignments)
673.188 Million cell updates/sec

Title: US-10-655-801-20

Perfect score: 18

Sequence: 1 cgtctgaactgcccag 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11282798

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA.Main:*
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	9	US-10-182-049-20
2	15.4	85.6	22	8	US-10-508-863-7
3	15.4	85.6	25	8	US-10-719-900-409560
4	14.8	82.2	25	7	US-10-719-956-464843
5	14.8	82.2	25	7	US-10-719-956-596880
6	14.8	82.2	25	8	US-10-719-900-647319
7	14.8	82.2	76	5	US-10-043-487-70
8	14.4	80.0	25	7	US-10-719-956-44720
9	14.4	80.0	25	7	US-10-719-956-199852
10	14.4	80.0	25	7	US-10-719-956-425140
11	14.4	80.0	25	7	US-10-719-956-506614
12	14.4	80.0	25	7	US-10-719-956-563766
13	14	77.8	25	8	US-10-719-900-463026
14	14	77.8	25	8	US-10-719-900-492613
15	14	77.8	25	10	US-11-036-317-789153
16	13.8	76.7	25	7	US-10-719-956-30344
17	13.8	76.7	25	7	US-10-719-956-433626
18	13.8	76.7	25	7	US-10-719-956-566856
19	13.8	76.7	25	7	US-10-719-956-637106
20	13.8	76.7	25	7	US-10-719-956-683368
21	13.8	76.7	25	7	US-10-719-956-687023
22	13.8	76.7	25	8	US-10-719-900-3641
23	13.8	76.7	25	8	US-10-719-900-391493

24	13.8	76.7	25	8	US-10-719-900-409559	Sequence 409559,
25	13.8	76.7	25	8	US-10-719-900-714062	Sequence 714062,
26	13.8	76.7	25	9	US-10-956-157-160516	Sequence 160516,
27	13.8	76.7	25	9	US-10-956-157-210346	Sequence 210346,
28	13.8	76.7	25	9	US-10-956-157-256211	Sequence 256211,
29	13.8	76.7	25	9	US-10-956-157-291756	Sequence 291756,
30	13.8	76.7	25	10	US-11-036-317-821377	Sequence 821377,
31	13.8	76.7	25	10	US-11-060-756-188296	Sequence 188296,
32	13.8	76.7	65	3	US-09-908-975-27383	Sequence 27383, A
33	13.4	74.4	20	7	US-10-280-183A-211	Sequence 211, App
34	13.4	74.4	25	7	US-10-719-956-205839	Sequence 205839,
35	13.4	74.4	25	7	US-10-719-956-454386	Sequence 454386,
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37	13.4	74.4	25	8	US-10-719-900-131894	Sequence 131894,
38	13.4	74.4	25	8	US-10-719-900-192759	Sequence 192759,
39	13.4	74.4	25	8	US-10-719-900-613650	Sequence 613650,
40	13.4	74.4	25	8	US-10-719-900-722102	Sequence 722102,
41	13.4	74.4	25	8	US-10-719-900-819672	Sequence 819672,
42	13.4	74.4	25	9	US-10-809-189-5801	Sequence 5801, App
43	13.4	74.4	25	9	US-10-809-189-5802	Sequence 5802, App
44	13.4	74.4	25	9	US-10-956-157-164909	Sequence 164909,
45	13.4	74.4	30	5	US-10-053-883-49	Sequence 49, Appl
46	13.4	74.4	60	3	US-09-908-975-16857	Sequence 16857, A
47	13.2	73.3	20	7	US-10-303-420-73	Sequence 73, Appl
48	13.2	73.3	25	5	US-10-098-263B-78012	Sequence 78012, A
49	13.2	73.3	25	7	US-10-719-956-159349	Sequence 159349,
50	13.2	73.3	25	7	US-10-719-956-159350	Sequence 159350,
51	13.2	73.3	25	7	US-10-719-956-249505	Sequence 249505,
52	13.2	73.3	25	7	US-10-719-956-464842	Sequence 464842,
53	13.2	73.3	25	7	US-10-719-956-596881	Sequence 596881,
54	13.2	73.3	25	8	US-10-719-900-55893	Sequence 55893, A
55	13.2	73.3	25	8	US-10-719-900-268396	Sequence 268396,
56	13.2	73.3	25	8	US-10-719-900-305146	Sequence 305146,
57	13.2	73.3	25	8	US-10-719-900-305147	Sequence 305147,
58	13.2	73.3	25	8	US-10-719-900-427474	Sequence 427474,
59	13.2	73.3	25	8	US-10-719-900-447134	Sequence 447134,
60	13.2	73.3	25	8	US-10-719-900-447135	Sequence 447135,
61	13.2	73.3	25	8	US-10-719-900-474762	Sequence 474762,
62	13.2	73.3	25	8	US-10-719-900-647318	Sequence 647318,
63	13.2	73.3	25	8	US-10-719-900-730151	Sequence 730151,
64	13.2	73.3	25	8	US-10-719-900-831370	Sequence 831370,
65	13.2	73.3	25	8	US-10-719-900-831371	Sequence 831371,
66	13.2	73.3	25	8	US-10-719-900-834909	Sequence 834909,
67	13.2	73.3	25	9	US-10-809-189-29403	Sequence 29403, A
68	13.2	73.3	25	9	US-10-809-189-29404	Sequence 29404, A
69	13.2	73.3	25	9	US-10-809-189-113025	Sequence 113025,
70	13.2	73.3	25	9	US-10-956-157-197861	Sequence 197861,
71	13.2	73.3	25	9	US-10-956-157-198885	Sequence 198885,
72	13.2	73.3	25	9	US-10-956-157-217325	Sequence 217325,
73	13.2	73.3	25	10	US-11-036-317-38997	Sequence 38997, A
74	13.2	73.3	25	10	US-11-036-317-83526	Sequence 83526, A
75	13.2	73.3	25	10	US-11-036-317-412135	Sequence 412135,
76	13.2	73.3	25	10	US-11-036-317-446749	Sequence 446749,
77	13.2	73.3	25	10	US-11-036-317-587286	Sequence 587286,
78	13.2	73.3	25	10	US-11-036-317-618048	Sequence 618048,
79	13.2	73.3	25	10	US-11-036-317-695245	Sequence 695245,
80	13.2	73.3	25	10	US-11-036-317-808950	Sequence 808950,
81	13.2	73.3	25	10	US-11-060-756-116937	Sequence 116937,
82	13.2	73.3	25	10	US-11-060-756-156473	Sequence 156473,
83	13.2	73.3	25	10	US-11-060-756-202905	Sequence 202905,
84	13.2	73.3	25	10	US-11-060-756-258462	Sequence 258462,
85	13.2	73.3	25	10	US-11-060-756-263749	Sequence 263749,
86	13.2	73.3	25	10	US-11-060-756-273810	Sequence 273810,
87	13.2	73.3	37	5	US-10-068-851-12	Sequence 12, Appl
88	13.2	73.3	50	6	US-10-131-827-4758	Sequence 4758, App
89	13.2	73.3	60	3	US-09-908-975-8230	Sequence 8230, App
90	13.2	73.3	65	3	US-09-908-975-12817	Sequence 12817, A
91	13.2	73.3	65	3	US-09-908-975-27016	Sequence 27016, A
92	13.2	73.3	65	3	US-09-908-975-28832	Sequence 28832, A
93	13	72.2	25	7	US-10-719-956-265514	Sequence 265514,
94	13	72.2	25	7	US-10-719-956-329291	Sequence 329291,
95	13	72.2	25	8	US-10-719-900-915056	Sequence 915056,
96	12.8	71.1	17	3	US-09-792-818-655	Sequence 655, App

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c 97 12.8 71.1 18 6 US-10-297-068-388 Sequence 388, App
c 98 12.8 71.1 18 6 US-10-297-068-389 Sequence 389, App
99 12.8 71.1 20 6 US-10-331-907-76 Sequence 76, Appl
100 12.8 71.1 23 6 US-10-184-282-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-182-049-20
; Sequence 20, Application US/10182049
; Publication No. US20050113322A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSION
; FILE REFERENCE: RSP-0360
; CURRENT APPLICATION NUMBER: US/10/182,049
; CURRENT FILING DATE: 2002-07-27
; PRIOR APPLICATION NUMBER: 09/490,208
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-182-049-20

Query Match 100.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCG 18
DB 1 CTGCTAGAACTGCCCG 18

RESULT 2
US-10-608-863-7
; Sequence 7, Application US/10608863
; Publication No. US20040214192A1
; GENERAL INFORMATION:
; APPLICANT: Hashida, Ryochi
; APPLICANT: Kagawa, Shinji
; APPLICANT: Yayoi, Yoshihiro
; APPLICANT: Sugita, Yuji
; APPLICANT: Saito, Hirohisa
; TITLE OF INVENTION: METHODS FOR EXAMINATION FOR ALLERGIC DISEASES, AND DRUGS FOR TREATING ALLERGIC DISEASES
; FILE REFERENCE: 3462.1003-000
; CURRENT APPLICATION NUMBER: US/10/608,863
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: JP 2002-188490
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Artificially Synthesized Primer Sequence
US-10-608-863-7

Query Match 85.6%; Score 15.4; DB 8; Length 22;
Best Local Similarity 94.1%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 2 TGTCTAGAACTGCCCG 18
DB 6 TGTCTAGAACTGCCCG 22

RESULT 3
US-10-719-900-409560
; Sequence 409560, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 409560
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-409560

Query Match 85.6%; Score 15.4; DB 8; Length 25;
Best Local Similarity 94.1%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCG 17
DB 8 CTGCTAGAACTGCCCG 24

RESULT 4
US-10-719-956-464843
; Sequence 464843, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,936
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 464843
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-464843

Query Match 82.2%; Score 14.8; DB 7; Length 25;
Best Local Similarity 88.9%; Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCG 18
DB 8 CTCTTAGAAGTGCCCG 25

RESULT 5
US-10-719-956-596880/c
; Sequence 596880, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
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; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,836
 ; PRIOR FILING DATE: 2002 11 20
 ; NUMBER OF SEQ ID NOS: 699466
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 596880
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 US-10-719-956-596880

Query Match 82.2%; Score 14.8; DB 7; Length 25;
 Best Local Similarity 88.9%; Pred. No. 4.7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCG 18
 |||||
 Db 24 CTGCTAGAACTGCCCG 7

RESULT 6
 US-10-719-900-647319
 ; Sequence 647319, Application US/10719900
 ; Publication No. US20050026164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002 11 20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 647319
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-719-900-647319

Query Match 82.2%; Score 14.8; DB 8; Length 25;
 Best Local Similarity 88.9%; Pred. No. 4.7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCG 18
 |||||
 Db 8 CTCTAGAACTGCCCG 25

RESULT 7
 US-10-043-487-70
 ; Sequence 70, Application US/10043487
 ; Publication No. US20030055220A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PIERRE, LEGRAIN
 ; TITLE OF INVENTION: Protein-protein interactions between Shigella flexneri polypeptides
 ; FILE REFERENCE: B4778A
 ; CURRENT APPLICATION NUMBER: US/10/043,487
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/261,130
 ; PRIOR FILING DATE: 2001-01-12
 ; NUMBER OF SEQ ID NOS: 561
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 70
 ; LENGTH: 76
 ; TYPE: DNA
 ; ORGANISM: Shigella flexneri
 US-10-043-487-70

Query Match 82.2%; Score 14.8; DB 5; Length 76;
 Best Local Similarity 88.9%; Pred. No. 4.9e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CTGCTAGAACTGCCCG 18
 |||||
 Db 20 CTCTAGAACTGCCCG 37

RESULT 8
 US-10-719-956-44720
 ; Sequence 44720, Application US/10719956
 ; Publication No. US20040146910A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
 ; FILE REFERENCE: 3527.1
 ; CURRENT APPLICATION NUMBER: US/10/719,956
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,836
 ; PRIOR FILING DATE: 2002 11 20
 ; NUMBER OF SEQ ID NOS: 699466
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 44720
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 US-10-719-956-44720

Query Match 80.0%; Score 14.4; DB 7; Length 25;
 Best Local Similarity 93.8%; Pred. No. 7.9e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCG 16
 |||||
 Db 6 CTGCTAGAACTGCCCG 21

RESULT 9
 US-10-719-956-199852/c
 ; Sequence 199852, Application US/10719956
 ; Publication No. US20040146910A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
 ; FILE REFERENCE: 3527.1
 ; CURRENT APPLICATION NUMBER: US/10/719,956
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,836
 ; PRIOR FILING DATE: 2002 11 20
 ; NUMBER OF SEQ ID NOS: 699466
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 199852
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 US-10-719-956-199852

Query Match 80.0%; Score 14.4; DB 7; Length 25;
 Best Local Similarity 93.8%; Pred. No. 7.9e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCG 16
 |||||
 Db 22 CTGCTAGAACTGCCCG 7

RESULT 10
 US-10-719-956-425140
 ; Sequence 425140, Application US/10719956
 ; Publication No. US20040146910A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
 ; FILE REFERENCE: 3527.1

; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 425140
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-425140

Query Match 80.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 7.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCC 16
Db 9 CTGTCCAGAACTGCC 24

RESULT 11

US-10-719-956-506614/c
; Sequence 506614, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 506614
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-506614

Query Match 80.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 7.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCC 16
Db 16 CTGTCTAGAACTGCAC 1

RESULT 12

US-10-719-956-563766
; Sequence 563766, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 563766
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-563766

Query Match 80.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 7.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCTAGAACTGCCCA 17
Db 4 TGCTAGAACTGCCCA 19

RESULT 13

US-10-719-900-463026/c
; Sequence 463026, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 463026
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-463026

Query Match 77.8%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTAGAACTGCCCAG 18
Db 16 CTAGAACTGCCCAG 3

RESULT 14

US-10-719-900-492613/c
; Sequence 492613, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 492613
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-492613

Query Match 77.8%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCTAGAACTGCCCA 17
Db 20 TCTAGAACTGCCCA 7

RESULT 15

US-11-036-317-789153/c
; Sequence 789153, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1

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; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 789153
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-789153

Query Match          77.8%; Score 14; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTAGAACTGCCAG 18
Db 15 CTAGAACTGCCAG 2

RESULT 16
US-10-719-956-30344
; Sequence 30344, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 30344
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-30344

Query Match          76.7%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCA 17
Db 6 CTGCTTAGAACTGCACA 22

RESULT 17
US-10-719-956-433626
; Sequence 433626, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 433626
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-433626

Query Match          76.7%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 2 TGTCTAGAACTGCCAG 18
Db 4 TGTCTACAACAGCCAG 20

RESULT 18
US-10-719-956-566856/c
; Sequence 566856, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 566856
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-566856

Query Match          76.7%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGTCTAGAACTGCCAG 18
Db 23 TTTCTAGAACTTCCAG 7

RESULT 19
US-10-719-956-637106/c
; Sequence 637106, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 637106
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-637106

Query Match          76.7%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCA 17
Db 17 CTGCTAGATCTGCCA 1

RESULT 20
US-10-719-956-683368
; Sequence 683368, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
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; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 714062
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-714062

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Query Match      76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      2 TGTCTAGAACTGCCCG 18
      ||| ||||| |||
Db      23 TGTGTAGAACTGTCCAG 7

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Job time : 222.11 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:35:12 ; Search time 97.8559 Seconds
(without alignments)
403.294 Million cell updates/sec

Title: US-10-655-801-20

Perfect score: 18

Sequence: 1 ctgtctagaactgcccag 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096243582 residues

Total number of hits satisfying chosen parameters: 11869656

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA.New.*
1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.8	82.2	25	12	US-11-121-849-107523
2	14.8	82.2	25	12	US-11-136-527-339204
3	13.8	76.7	22	8	US-10-310-914A-925402
4	13.8	76.7	25	12	US-11-121-849-9721
5	13.8	76.7	25	12	US-11-121-849-297925
6	13.8	76.7	25	12	US-11-121-849-366615
7	13.8	76.7	25	12	US-11-136-527-127254
8	13.8	76.7	25	12	US-11-136-527-321780
9	13.8	76.7	25	12	US-11-136-527-330649
10	13.8	76.7	50	12	US-11-175-859-98954
11	13.4	74.4	19	8	US-10-310-914A-1209005
12	13.4	74.4	19	10	US-11-101-244-47652
13	13.4	74.4	19	10	US-11-101-244-365369
14	13.4	74.4	19	10	US-11-101-244-978416
15	13.4	74.4	19	11	US-11-083-784-47652
16	13.4	74.4	19	11	US-11-083-784-365369
17	13.4	74.4	19	11	US-11-083-784-978416
18	13.4	74.4	21	8	US-10-310-914A-535346
19	13.4	74.4	22	8	US-10-310-914A-497795
20	13.4	74.4	25	12	US-11-121-849-76084

Sequence 76085, A	25	12	US-11-121-849-76085	74.4	c 21
Sequence 360704,	25	12	US-11-121-849-360704	74.4	c 22
Sequence 116504,	25	12	US-11-136-527-116504	74.4	c 23
Sequence 116505,	25	12	US-11-136-527-116505	74.4	c 24
Sequence 235336,	25	12	US-11-136-527-235336	74.4	c 25
Sequence 49, Appl	30	12	US-11-193-528-49	74.4	c 26
Sequence 3381, Ap	50	12	US-11-175-859-3381	74.4	c 27
Sequence 15438, A	50	12	US-11-175-859-15438	74.4	c 28
Sequence 456967,	20	8	US-10-310-914A-456967	73.3	c 29
Sequence 611488,	22	8	US-10-310-914A-611488	73.3	c 30
Sequence 762370,	22	8	US-10-310-914A-762370	73.3	c 31
Sequence 357535,	24	8	US-10-310-914A-357535	73.3	c 32
Sequence 170920,	25	12	US-11-121-849-170920	73.3	c 33
Sequence 193150,	25	12	US-11-121-849-193150	73.3	c 34
Sequence 193194,	25	12	US-11-121-849-193194	73.3	c 35
Sequence 276262,	25	12	US-11-121-849-276262	73.3	c 36
Sequence 357010,	25	12	US-11-121-849-357010	73.3	c 37
Sequence 517451,	25	12	US-11-121-849-517451	73.3	c 38
Sequence 672213,	25	12	US-11-121-849-672213	73.3	c 39
Sequence 672541,	25	12	US-11-121-849-672541	73.3	c 40
Sequence 672542,	25	12	US-11-121-849-672542	73.3	c 41
Sequence 339707,	25	12	US-11-136-527-339707	73.3	c 42
Sequence 339726,	25	12	US-11-136-527-339726	73.3	c 43
Sequence 12, Appl	37	12	US-11-002-141-12	73.3	c 44
Sequence 13907, A	68	8	US-10-310-914A-13907	73.3	c 45
Sequence 9432, Ap	74	8	US-10-310-914A-9432	73.3	c 46
Sequence 4844, Ap	79	8	US-10-310-914A-4844	73.3	c 47
Sequence 535341,	23	8	US-10-310-914A-535341	72.2	c 48
Sequence 439332,	23	8	US-10-310-914A-439332	71.1	c 49
Sequence 1307598,	18	8	US-10-310-914A-1307598	71.1	c 50
Sequence 156956,	19	10	US-11-101-244-156956	71.1	c 51
Sequence 289621,	19	10	US-11-101-244-289621	71.1	c 52
Sequence 466854,	19	10	US-11-101-244-466854	71.1	c 53
Sequence 783242,	19	10	US-11-101-244-783242	71.1	c 54
Sequence 865598,	19	10	US-11-101-244-865598	71.1	c 55
Sequence 865610,	19	10	US-11-101-244-865610	71.1	c 56
Sequence 156956,	19	11	US-11-083-784-156956	71.1	c 57
Sequence 289621,	19	11	US-11-083-784-289621	71.1	c 58
Sequence 466854,	19	11	US-11-083-784-466854	71.1	c 59
Sequence 783242,	19	11	US-11-083-784-783242	71.1	c 60
Sequence 865598,	19	11	US-11-083-784-865598	71.1	c 61
Sequence 865610,	19	11	US-11-083-784-865610	71.1	c 62
Sequence 418107,	20	8	US-10-310-914A-418107	71.1	c 63
Sequence 461469,	21	8	US-10-310-914A-461469	71.1	c 64
Sequence 667101,	21	8	US-10-310-914A-667101	71.1	c 65
Sequence 925422,	22	8	US-10-310-914A-925422	71.1	c 66
Sequence 362001,	23	8	US-10-310-914A-362001	71.1	c 67
Sequence 667116,	23	8	US-10-310-914A-667116	71.1	c 68
Sequence 979076,	24	8	US-10-310-914A-979076	71.1	c 69
Sequence 39028, A	25	12	US-11-121-849-39028	71.1	c 70
Sequence 43680, A	25	12	US-11-121-849-43680	71.1	c 71
Sequence 11621,	25	12	US-11-121-849-11621	71.1	c 72
Sequence 170075,	25	12	US-11-121-849-170075	71.1	c 73
Sequence 366614,	25	12	US-11-121-849-366614	71.1	c 74
Sequence 419603,	25	12	US-11-121-849-419603	71.1	c 75
Sequence 61681, A	25	12	US-11-136-527-61681	71.1	c 76
Sequence 258001,	25	12	US-11-136-527-258001	71.1	c 77
Sequence 258022,	25	12	US-11-136-527-258022	71.1	c 78
Sequence 336361,	25	12	US-11-136-527-336361	71.1	c 79
Sequence 34375, A	50	12	US-11-175-859-34375	71.1	c 80
Sequence 40946, A	50	12	US-11-175-859-40946	71.1	c 81
Sequence 671437,	19	8	US-10-310-914A-671437	68.9	c 82
Sequence 184742,	19	10	US-11-101-244-184742	68.9	c 83
Sequence 352338,	19	10	US-11-101-244-352338	68.9	c 84
Sequence 525775,	19	10	US-11-101-244-525775	68.9	c 85
Sequence 865634,	19	10	US-11-101-244-865634	68.9	c 86
Sequence 867750,	19	10	US-11-101-244-867750	68.9	c 87
Sequence 867777,	19	10	US-11-101-244-867777	68.9	c 88
Sequence 147150,	19	10	US-11-101-244-147150	68.9	c 89
Sequence 184742,	19	11	US-11-083-784-184742	68.9	c 90
Sequence 352338,	19	11	US-11-083-784-352338	68.9	c 91
Sequence 525775,	19	11	US-11-083-784-525775	68.9	c 92
Sequence 525775,	19	11	US-11-083-784-525775	68.9	c 93

c 94 12.4 68.9 19 11 US-11-083-784-865634 Sequence 865634,
c 95 12.4 68.9 19 11 US-11-083-784-867750 Sequence 867750,
c 96 12.4 68.9 19 11 US-11-083-784-867777 Sequence 867777,
c 97 12.4 68.9 19 11 US-11-083-784-1417150 Sequence 1417150,
c 98 12.4 68.9 20 8 US-10-310-914A-782986 Sequence 782986,
c 99 12.4 68.9 21 8 US-10-310-914A-361952 Sequence 361952,
c 100 12.4 68.9 23 8 US-10-310-914A-782849 Sequence 782849,

ALIGNMENTS

RESULT 1

US-11-121-849-107523
; Sequence 107523, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 107523
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-107523

Query Match 82.2%; Score 14.8; DB 12; Length 25;
Best Local Similarity 88.9%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCCG 18
||| ||||| ||||| |||||
Db 8 CTTTCTAGAAATGCCCG 25

RESULT 2

US-11-136-527-339204/c
; Sequence 339204, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 339204
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-339204

Query Match 82.2%; Score 14.8; DB 12; Length 25;
Best Local Similarity 88.9%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCCG 18
||| ||||| ||||| |||||
Db 23 CTGGCTAGATCTGCCCG 6

RESULT 3

US-10-310-914A-925402/c
; Sequence 925402, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 925402
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-925402

Query Match 76.7%; Score 13.8; DB 8; Length 22;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGTCTAGAACTGCCCG 18
||| ||||| ||||| |||||
Db 17 TTTCTAGTACTGCCCG 1

RESULT 4

US-11-121-849-9721
; Sequence 9721, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 9721
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-9721

Query Match 76.7%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGTCTAGAACTGCCCG 18
||| ||||| ||||| |||||
Db 3 TGTCTAACTGCCTAG 19

RESULT 5

US-11-121-849-297925
; Sequence 297925, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03

; NUMBER OF SEQ ID NOS: 673904
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 297925
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-11-121-849-297925

Query Match 76.7%; Score 13.8; DB 12; Length 25;
 Best Local Similarity 88.2%; Pred. No. 2.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCTAGAACTGCCAG 18
 |||||
 Db 7 TTCTAGTACTGCCAG 23

RESULT 6
 US-11-121-849-366615
 ; Sequence 366615, Application US/11121849
 ; Publication No. US20050272080A1
 ; GENERAL INFORMATION:
 ; APPLICANT: John Palma
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
 ; TYPE OF INVENTION: Microarrays
 ; FILE REFERENCE: 3684.1
 ; CURRENT APPLICATION NUMBER: US/11/121,849
 ; CURRENT FILING DATE: 2005-05-03
 ; PRIOR APPLICATION NUMBER: 60/567,949
 ; PRIOR FILING DATE: 2004-05-03
 ; NUMBER OF SEQ ID NOS: 673904
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 366615
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-11-121-849-366615

Query Match 76.7%; Score 13.8; DB 12; Length 25;
 Best Local Similarity 88.2%; Pred. No. 2.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCTAGAACTGCCAG 18
 |||||
 Db 6 TGGCTGGAAGTGCACG 22

RESULT 7
 US-11-136-527-127254
 ; Sequence 127254, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/574,294
 ; PRIOR FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 127254
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Probe
 US-11-136-527-127254

Query Match 76.7%; Score 13.8; DB 12; Length 25;
 Best Local Similarity 88.2%; Pred. No. 2.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCA 17
 |||||
 Db 4 CTGCTAGAACTTCCA 20

RESULT 8
 US-11-136-527-321780/c
 ; Sequence 321780, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/574,294
 ; PRIOR FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 321780
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Probe
 US-11-136-527-321780

Query Match 76.7%; Score 13.8; DB 12; Length 25;
 Best Local Similarity 88.2%; Pred. No. 2.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCA 17
 |||||
 Db 24 CTGCTGGAAGTGCCCA 8

RESULT 9
 US-11-136-527-330649
 ; Sequence 330649, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/574,294
 ; PRIOR FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 330649
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Probe
 US-11-136-527-330649

Query Match 76.7%; Score 13.8; DB 12; Length 25;
 Best Local Similarity 88.2%; Pred. No. 2.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCCA 17
 |||||
 Db 3 CTGCTAGAACTTCCA 19

RESULT 10
 US-11-175-859-98954
 ; Sequence 98954, Application US/11175859

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; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US/11/175,859
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 98954
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-98954

Query Match          76.7%; Score 13.8; DB 12; Length 50;
Best Local Similarity 88.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGTCTAGAACTGCCCA 17
   ||||| |||||
Db 32 CTGTCTACCACTGCCCA 48

RESULT 11
US-10-310-914A-1209005
; Sequence 1209005, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1209005
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1209005

Query Match          74.4%; Score 13.4; DB 8; Length 19;
Best Local Similarity 73.3%; Pred. No. 4.7e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTAGAACTGCCCA 18
   :||| :|||
Db 5 UCUAGACCGCCAG 19

RESULT 12
US-11-101-244-47652
; Sequence 47652, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
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; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 47652
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-47652

Query Match          74.4%; Score 13.4; DB 10; Length 19;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTCTAGAACTGCCCA 17
   |:| |||||:|
Db 1 GUCCAGAACUGCCCA 15

RESULT 13
US-11-101-244-365369
; Sequence 365369, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 365369
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-365369

Query Match          74.4%; Score 13.4; DB 10; Length 19;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTCTAGAACTGCCCA 17
   |:| |||||:|
Db 1 GUCCAGAACUGCCCA 15

RESULT 14
US-11-101-244-978416/c
; Sequence 978416, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
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; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 978416
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-978416

Query Match 74.4%; Score 13.4; DB 10; Length 19;
 Best Local Similarity 93.3%; Pred. No. 4.7e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCC 15
 Db 18 CTGTGTAAGCTGCC 4

RESULT 15
 US-11-083-784-47652
 ; Sequence 47652, Application US/11083784
 ; Publication No. US20050245475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/083,784
 ; CURRENT FILING DATE: 2005-03-18
 ; PRIOR APPLICATION NUMBER: US/10/714,333
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 47652
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-083-784-47652

Query Match 74.4%; Score 13.4; DB 11; Length 19;
 Best Local Similarity 80.0%; Pred. No. 4.7e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3.GTCTAGAACTGCCA 17
 Db 1 GUCCAGAACUGCCCA 15

RESULT 16
 US-11-083-784-365369
 ; Sequence 365369, Application US/11083784
 ; Publication No. US20050245475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/083,784
 ; CURRENT FILING DATE: 2005-03-18
 ; PRIOR APPLICATION NUMBER: US/10/714,333
 ; PRIOR FILING DATE: 2003-11-14

; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 365369
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-083-784-365369

Query Match 74.4%; Score 13.4; DB 11; Length 19;
 Best Local Similarity 80.0%; Pred. No. 4.7e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GTCTAGAACTGCCA 17
 Db 1 GUCCAGAACUGCCCA 15

RESULT 17
 US-11-083-784-978416/C
 ; Sequence 978416, Application US/11083784
 ; Publication No. US20050245475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/083,784
 ; CURRENT FILING DATE: 2005-03-18
 ; PRIOR APPLICATION NUMBER: US/10/714,333
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 978416
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-083-784-978416

Query Match 74.4%; Score 13.4; DB 11; Length 19;
 Best Local Similarity 93.3%; Pred. No. 4.7e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCC 15
 Db 18 CTGTGTAAGCTGCC 4

RESULT 18
 US-10-310-914A-535346
 ; Sequence 535346, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shiller, Kvyuzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: Patent in version 3.3

; SEQ ID NO 535346
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-535346

Query Match 74.4%; Score 13.4; DB 8; Length 21;
Best Local Similarity 73.3%; Pred. No. 4.8e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCTAGAACTCCCG 18
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Db 3 UCUGAACUGCCUG 17

RESULT 19

US-10-310-914A-497795
; Sequence 497795, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 497795
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-497795

Query Match 74.4%; Score 13.4; DB 8; Length 22;
Best Local Similarity 73.3%; Pred. No. 4.8e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCTAGAACTCCCG 18
: : ||||| :
Db 1 UCUGAACUGCCCG 15

RESULT 20

US-11-121-849-76084/c
; Sequence 76084, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 76084
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-76084

Query Match 74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCC 15
: : ||||| :
Db 23 CTGTCTAGAACTGCC 9

RESULT 21

US-11-121-849-76085/c
; Sequence 76085, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 76085
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-76085

Query Match 74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCC 15
: : ||||| :
Db 17 CTGTCTAGAACTGCC 3

RESULT 22

US-11-121-849-360704/c
; Sequence 360704, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 360704
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-360704

Query Match 74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGTCTAGAACTGCC 15
: : ||||| :
Db 18 CTGTCTAGAACTGCC 4

RESULT 23

US-11-136-527-116504/c
; Sequence 116504, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294

; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 116504
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-116504

Query Match 74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCC 15
|||
DB 19 CTGCTAGAACTGCC 5

RESULT 24

US-11-136-527-116505/c
; Sequence 116505, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 116505
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-116505

Query Match 74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCC 15
|||
DB 16 CTGCTAGAACTGCC 2

RESULT 25

US-11-136-527-235336/c
; Sequence 235336, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 235336
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe

US-11-136-527-235336

Query Match 74.4%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGTCTAGAACTGCC 16
|||
DB 21 TGTATAGAACTGCC 7

Search completed: March 3, 2006, 07:56:43
Job time: 98.0559 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:25:53 ; Search time 984.737 Seconds
(without alignments)
855.220 Million cell updates/sec

Title: US-10-655-801-20

Perfect score: 18

Sequence: 1 ctgtctagaactgcccag 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 512758

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gse1:*

10: gb_gse2:*

11: gb_gse3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.4	74.4	58	8	DR104908 JHU075B06
2	13.4	74.4	65	5	BU947098 rf19b05.y
3	13.2	73.3	61	9	CC591222 CH240.391
4	13.2	73.3	77	1	AI903025 QV-BT022-
5	13.2	73.3	80	1	AJ649674 AJ649674
6	12.8	71.1	68	10	CW156639 104_559.1
7	12.8	71.1	68	10	CW156640 104_559.1
8	12.8	71.1	70	10	BX145365
9	12.8	71.1	71	1	AL794076
10	12.8	71.1	77	1	AA045040
11	12.4	68.9	35	6	CF642114 D47_H04_F
12	12.4	68.9	65	6	CD967875 SEY_37_Ge
13	12.4	68.9	80	11	CR136088
14	12.2	67.8	67	9	BZ594304 SALK_0837
15	12.2	67.8	70	1	AA118970
16	12.2	67.8	72	10	CL639237
17	12.2	67.8	73	1	AI941463
18	12.2	67.8	73	1	AL850449
19	12.2	67.8	73	7	CK725727
20	12.2	67.8	73	9	AZ663394
21	12.2	67.8	78	2	BG749927
22	12.2	67.8	78	9	AZ663149

C	23	12.2	67.8	80	2	BG868495
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C	25	12	66.7	77	3	BJ034925
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C	27	11.8	65.6	40	1	AI443492
C	28	11.8	65.6	44	3	BJ080392
C	29	11.8	65.6	53	2	BE381108
C	30	11.8	65.6	57	9	BZ287795
C	31	11.8	65.6	61	1	AA503563
C	32	11.8	65.6	62	5	AX714068
C	33	11.8	65.6	64	1	AA004529
C	34	11.8	65.6	67	1	AI791108
C	35	11.8	65.6	69	2	BG862449
C	36	11.8	65.6	73	6	CF032281
C	37	11.8	65.6	73	9	AZ432961
C	38	11.8	65.6	77	11	DR35F23S
C	39	11.6	64.4	29	9	AZ309154
C	40	11.6	64.4	35	9	AZ658984
C	41	11.6	64.4	45	3	BJ035831
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C	43	11.6	64.4	49	10	BX291286
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C	53	11.6	64.4	66	9	BH234539
C	54	11.6	64.4	69	6	AZ768201
C	55	11.6	64.4	69	6	CD964541
C	56	11.6	64.4	70	3	BM442237
C	57	11.6	64.4	70	10	CG670830
C	58	11.6	64.4	72	1	AA109168
C	59	11.6	64.4	72	8	DR421668
C	60	11.6	64.4	72	11	CR045226
C	61	11.6	64.4	72	11	CR193035
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C	65	11.6	64.4	80	2	BE375856
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C	67	11.6	64.4	82	10	CW048142
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C	76	11.4	63.3	76	3	BJ000310
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C	79	11.2	62.2	26	9	AZ660695
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C	81	11.2	62.2	41	9	AZ779709
C	82	11.2	62.2	42	1	AJ651067
C	83	11.2	62.2	46	1	AJ650474
C	84	11.2	62.2	46	1	AJ650474
C	85	11.2	62.2	46	1	BH642092
C	86	11.2	62.2	50	7	CK722738
C	87	11.2	62.2	52	7	CF973423
C	88	11.2	62.2	52	7	CN849195
C	89	11.2	62.2	52	8	CW830501
C	90	11.2	62.2	52	8	CC533924
C	91	11.2	62.2	53	8	DN252645
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C	95	11.2	62.2	58	1	AA522220

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AA004529	zh91a10.r
AI791108	uk55910.y
BG862449	602796178
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AZ432961	1M0218P05
AL975765	Danilo.rer
AZ309154	1M0013A20
AZ658984	1M0536N03
DR107372	JHU138B12
BJ035831	BJ035831
AX488169	T. brucei
BX291286	Arabidops
AU107182	AU107182
CR144072	Reverse.s
CZ906313	BC0210.Sa
CZ42770	IBB16B10.
BX289316	Arabidops
CG581377	OST221623
AZ828943	2M0106H18
CF934611	TREST-B15
CW501173	fbb5001f2
BH234539	1006179G0
AZ768201	1M0568N04
CD964541	SEC_7.Gen
BM442237	Eban01.SQ
CG670830	OST471681
AA109168	mp38f03.r
DR421668	nav01h08.
CR045226	Forward.s
CR193035	Reverse.s
BF639921	NP018C071
AA105826	mp04712.r
AG190245	Pan.trog1
BE375856	601229672
BH221619	1006102C0
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CN930230	00032AFB
CC178509	NPX427.Ba
CD944738	RDN_68.Ge
CD957496	SCJ_119.G
T75130	YC87f08.r1
CG583039	OST224808
CD942703	RCB_67.Ge
BJ000310	BJ000310
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AZ633973	1M0489H09
AZ660695	1M0538K22
AZ826498	2M0102N19
AZ779709	2M0016O20
AJ651067	AJ651067
AJ650474	vt90c03.r
AJ650474	AJ650474
BH642092	100805880
CK722738	jab15h02.
CF973423	FSU_b1one
CN849195	000820AAF
CW830501	ID0ACC15C
CC533924	CH240_412
DN252645	ACAB-aaab6
CZ479073	e01268-5p
BH889771	3526_1_11
AJ670337	AJ670337
AA522220	v143b02.r

96 11.2 62.2 58 10 AL754659 AL754659 Arabidops
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 99 11.2 62.2 62 1 AI801122 AI801122 tob5d12.x
 c 100 11.2 62.2 62 1 AW064193 AW064193 SP0639 KR

ALIGNMENTS

RESULT 1
 DR104908
 LOCUS
 DEFINITION JHU075B06L58 Canine cardiovascular system biased cDNA Canis
 familiaris cDNA, mRNA sequence;
 ACCSSION DR104908
 VERSION DR104908.1 GI:67564263
 KEYWORDS EST.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 Canis.

REFERENCE 1 (bases 1 to 58)
 AUTHORS Disilvestre,D., Yung,C., Gao,Z., Farukhi,Y., Winslow,R.L. and
 Tomaseelli,G.F.
 TITLE Canine cardiovascular system biased cDNA sequences
 JOURNAL Unpublished (2005)
 COMMENT Contact: Gordon F. Tomaseelli
 Johns Hopkins University
 720 Rutland Avenue/Ross 844, Baltimore, MD 21205, USA
 Tel: 4109552774
 Fax: 4105022096
 Email: gtomase@jhmi.edu.

FEATURES

source

1. 58
 Location/Qualifiers
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /strain="Mixed"
 /db_xref="taxon:9615"
 /sex="Mixed"
 /clone_lib="Canine cardiovascular system biased cDNA"
 /notes="Organ: Mixed; Vector: pCDNA3.1; Site 1: EcoRI;
 Site 2: XhoI; Adult tissue from eye, lung, aorta,
 pulmonary artery and brain; neonatal tissue from liver,
 spleen, thymus, lung, kidney, aorta and brain; 50% is from
 cardiac tissues."

ORIGIN

Query Match 74.4%; Score 13.4; DB 8; Length 58;
 Best Local Similarity 93.3%; Pred. No. 3.3e+04;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCTGAACTGCC 16

Db 31 TGCTTGAAGTCC 45

RESULT 2
 BU947098
 LOCUS
 DEFINITION rf19b05.y1 Meloidogyne hapla J2 SL1 TOPO v1 Meloidogyne hapla cDNA
 s., mRNA sequence.

ACCSSION BU947098

VERSION BU947098.1 GI:24198163

KEYWORDS EST.

SOURCE Meloidogyne hapla

ORGANISM Meloidogyne hapla

Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.

REFERENCE 1 (bases 1 to 65)
 AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
 Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,

TITLE
JOURNAL
COMMENT

Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
 Teagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
 Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
 Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
 McCann,R., Waterston,R. and Wilson,R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone will not be made available due to an unidentified
 microbial contamination of the source material. The library was
 constructed by Claire Murphy and Dr. James McCarter at Washington
 University, St. Louis. J2 were provided by Dr. Valerie Williamson
 of the University of California at Davis
 (vmwilliamson@ucdavis.edu).

Putative full length read

The vector to vector length is 75

Seq primer: -40RP from Gibco.

FEATURES

source

1. 65

Location/Qualifiers

/organism="Meloidogyne hapla"

/mol_type="mRNA"

/db_xref="taxon:6305"

/dev_stage="J2"

/lab_host="DH10B"

/clone_lib="Meloidogyne hapla J2 SL1 TOPO v1"

/notes="Vector: pCRII-TOPO (Invitrogen); Site 1: EcoRI;
 Site 2: EcoRI; The library was constructed by Claire
 Murphy and Dr. James McCarter at Washington University,
 St. Louis. Oligo(df)-SL1 PCR based library. Meloidogyne
 hapla J2 cDNA PCR products of size >400 nucleotides
 containing SL1 on the 5' end and oligo(df) on the 3' end
 were non-directionally cloned into pCRII-TOPO(Invitrogen)
 following the TOPO TA cloning protocol. J2 were provided
 by Dr. Valerie Williamson of University of California at
 Davis (vmwilliamson@ucdavis.edu)."

ORIGIN

Query Match 74.4%; Score 13.4; DB 5; Length 65;
 Best Local Similarity 93.3%; Pred. No. 3.4e+04;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCTAGAACTGCC 18

Db 13 TCTACAACTGCC 27

RESULT 3

CC591222/c

LOCUS

DEFINITION

CH240_391K18.TARBAC13P2 CHORI-240 Bos taurus genomic clone

CH240_391K18, genomic survey sequence.

CC591222

VERSION

CC591222.1 GI:31948692

KEYWORDS GSS.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 61)

AUTHORS

Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,

Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M., Chiu,R.,

Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Jones,S.,

Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,

Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,

Dall'ymple,B.P. and Tellam,R.

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398

JOURNAL
COMMENT

Unpublished (2003)
Other_GSSs: CH240_391K18.T7
Contact: Rob Holt
Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4B6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 391 row: K column: 18
Seq primer: SP6
Class: BAC ends.

FEATURES
source

1. .61
Location/Qualifiers
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Hereford"
/db_xref="taxon:9913"
/clones="CH240_391K18"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/notes="Vector: pIARAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull LI Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 73.3%; Score 13.2; DB 9; Length 61;
Best Local Similarity 83.3%; Pred. No. 4.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCAG 18
|||||
Db 49 CGGTGAGACGCCAG 32

RESULT 4
AI903025

LOCUS AI903025 79 bp mRNA linear EST 30-MAR-2000
DEFINITION QV-BT022-070199-028_1 BT022 Homo sapiens cDNA, mRNA sequence.

ACCESSION AI903025
VERSION AI903025.1 GI:6493412
KEYWORDS EST.

SOURCE
Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 79)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED
COMMENT

10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922

FEATURES
source

1. .79
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="female"
/dev_stage="Adult"
/clone_lib="BT022"
/notes="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Query Match 73.3%; Score 13.2; DB 1; Length 79;
Best Local Similarity 83.3%; Pred. No. 4.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTGCTAGAACTGCCAG 18
|||||
Db 16 CTGCCAGAACTGCCAG 33

RESULT 5
AJ649674

LOCUS AJ649674 80 bp mRNA linear EST 07-JUL-2004
DEFINITION AJ649674 CSEQRAN19 Sus scrofa cDNA clone C0003273_C07, mRNA
sequence.

ACCESSION AJ649674
VERSION AJ649674.1 GI:49326519
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE
AUTHORS

1 (bases 1 to 80)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle

JOURNAL
COMMENT

Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector: pBlueScriptII (KS) R. Site1: EcoRI
R. Site2: NotI 5'. Seq Primer M13P Normalised library constructed
from pooled ovaries. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.ark-genomics.org.

FEATURES
source

1. .80
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0003273_C07"
/tissue_type="ovary"
/clone_lib="CSEQRAN19"

/note="Vector: pBlueScriptII (KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing; Normalised library
constructed from pooled ovaries"

```

ORIGIN
  Query Match      73.3%; Score 13.2; DB 1; Length 80;
  Best Local Similarity 83.3%; Pred. No. 4.5e+04;
  Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCAG 18
    |||||
Db 17 CTGCTAGAACTCCCTAG 34
    |||||

RESULT 6
CW156639/c
LOCUS
DEFINITION
104 559 11146794 116 36378 069 Sorghum methylation filtered library
(LibID: 104) Sorghum bicolor genomic clone 11146794, genomic survey
sequence.

ACCESSION
CW156639
VERSION
GI:54849186
KEYWORDS
Sorghum bicolor (sorghum)
SOURCE
Sorghum bicolor
ORGANISM
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE
1 (bases 1 to 68)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holsman,H., Roe,B.A., Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
Martienssen,R.A.
Sorghum genome sequencing by methylation filtration
PLOS Biol. 3 (1), e13 (2005)
15660154
COMMENT
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 559 row: 1 column: 18
Seq primer: T3 Reverse
Class: methylation filtered
High quality sequence stop: 68.
Location/Qualifiers
1..68
/mol_type="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone="11146794"
/clone_lib="Sorghum methylation filtered library (LibID:
104)"
/note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pBCSK(-) vector
and electroporated into E. coli cells. This is a
methylation filtered library."

FEATURES
source
1..68
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone="11146794"
/clone_lib="Sorghum methylation filtered library (LibID:
104)"
/note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pBCSK(-) vector
and electroporated into E. coli cells. This is a
methylation filtered library."

ORIGIN
  Query Match      71.1%; Score 12.8; DB 10; Length 68;
  Best Local Similarity 87.5%; Pred. No. 7.2e+04;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGCTAGAACTGCCCA 17
    |||||
Db 13 TGCTAGAACTCCACA 28
    |||||

RESULT 8
BX145365/c
LOCUS
DEFINITION
Danio rerio genomic clone DKEY-106H4, genomic survey sequence.
ACCESSION
BX145365
VERSION
GI:27976715
KEYWORDS
Sorghum bicolor (sorghum)
SOURCE
Danio rerio (zebrafish)
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 70)
Humphray,S.J., Huckle,E. and Durham,J.L.
Direct Submission
Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

Qy 2 TGCTAGAACTGCCCA 17
    |||||
Db 54 TGCTAGAACTCCACA 39
    |||||

RESULT 7
CW156640
LOCUS
DEFINITION
104 559 11146794 116 36378 069 Sorghum methylation filtered library
(LibID: 104) Sorghum bicolor genomic clone 11146794, genomic survey
sequence.

ACCESSION
CW156640
VERSION
GI:54849187
KEYWORDS
Sorghum bicolor (sorghum)
SOURCE
Sorghum bicolor
ORGANISM
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE
1 (bases 1 to 68)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holsman,H., Roe,B.A., Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
Martienssen,R.A.
Sorghum genome sequencing by methylation filtration
PLOS Biol. 3 (1), e13 (2005)
15660154
COMMENT
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 559 row: 1 column: 18
Seq primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 68.
Location/Qualifiers
1..68
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
/clone="11146794"
/clone_lib="Sorghum methylation filtered library (LibID:
104)"
/note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pBCSK(-) vector
and electroporated into E. coli cells. This is a
methylation filtered library."

ORIGIN
  Query Match      71.1%; Score 12.8; DB 10; Length 68;
  Best Local Similarity 87.5%; Pred. No. 7.2e+04;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGCTAGAACTGCCCA 17
    |||||
Db 13 TGCTAGAACTCCACA 28
    |||||

RESULT 8
BX145365/c
LOCUS
DEFINITION
Danio rerio genomic clone DKEY-106H4, genomic survey sequence.
ACCESSION
BX145365
VERSION
GI:27976715
KEYWORDS
Sorghum bicolor (sorghum)
SOURCE
Danio rerio (zebrafish)
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 70)
Humphray,S.J., Huckle,E. and Durham,J.L.
Direct Submission
Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

```

humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 106H4. 106H4 is
part of the Danokey BAC library created by R. Plasterk and N.V.
Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_reio/.

FEATURES

Location/Qualifiers
1..70
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-106H4"
/tissue_type="Testis"
/note="Vector pIndigoBAC-536"

ORIGIN

Query Match 71.1%; Score 12.8; DB 10; Length 70;
Best Local Similarity 87.5%; Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TGTCTAGAACTGCCCA 17
Db 64 TGTATAGAACTGGCCA 49

RESULT 9

AL794076/c
LOCUS
DEFINITION AL794076 XGC-neurula Xenopus tropicalis cDNA clone TNeu116a17 5',
mRNA sequence.

ACCESSION AL794076.2 GI:38315956

VERSION

KEYWORDS

SOURCE

ORGANISM

Xenopus tropicalis (western clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopus;
Xenopodinae; Xenopus; Silurana.

REFERENCE

1 (bases 1 to 71)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)

JOURNAL

On Jun 25, 2002 this sequence version replaced gi:21579780.

Contact: Taylor R

Sanger Institute

Hinxton, Cambridgeshire, CB10 1SA, UK

Email: trop@sanger.ac.uk

This sequence is from a Xenopus Gene Collection (XGC) library

constructed by Aaron M. Zorn.

cDNA was oligo dt primed from 5ug of poly A+ RNA from neurula.

EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the

5' end and NotI at the 3' end.

Host: pCS107; Site 1: EcoRI; Site 2: NotI

Vector: Escherichia coli DH10B

Sanger Xenopus tropicalis EST project 2001

TROPICALIS_SEQUENCE_ID: TNeu116a17.plcSP6

Sequencing primer: SP6.

Location/Qualifiers

1..71

/organism="Xenopus tropicalis"

/mol_type="mRNA"

/db_xref="taxon:8364"

/clone="TNeu116a17"

/dev_stage="neurula"

/lab_host="Escherichia coli DH10B"

/clone_lib="XGC-neurula"

/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA

was oligo dt primed from Sug of poly A+ RNA from neurula.

EcoRI-NotI cut cDNA was then ligated into pCS107 with

EcoRI at the 5' end and NotI at the 3' end."

ORIGIN

Query Match 71.1%; Score 12.8; DB 1; Length 71;
Best Local Similarity 87.5%; Pred. No. 7.3e+04;

Matches

14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TGTCTAGAACTGCCCA 17
Db 67 TGTCTAGAACTGCCCA 52

RESULT 10

AA045040/c

LOCUS

DEFINITION

AA045040

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 77)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.P., Chiapelli,B.,

Chisoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,

Hawkins,M., Hultman,M., Kucaba,I., Lacy,M., Le,M., Le,N.,

Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,

Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,

Trevaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.

and Marra,M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

8889549

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LML; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1819 Std Error: 0.00

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 62.

Location/Qualifiers

1..77

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3803366"

/db_xref="taxon:9606"

/clone="IMAGE:488779"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="Soares_pregnant_uterus_NbHPU"

/note="Organ: uterus; Vector: pT7T3-Pac; Site 1: Not I;

Site 2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dt) primer [5',

AACTGGAAGATTCGCGCGCTTTTTTTTTTTT 3',

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization. Library

constructed by M. Fatima Bonaldo."

ORIGIN

Query Match 71.1%; Score 12.8; DB 1; Length 77;
Best Local Similarity 87.5%; Pred. No. 7.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CTTCTAGAACTGGCC 16
Db 44 CTTCTAGAACTGGCC 29

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RESULT 11
LOCUS CF642114/c
DEFINITION D47_H04 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
sequence.
ACCESSION CF642114
VERSION CF642114.1 GI:37409193
KEYWORDS EST.
SOURCE Ustilago maydis
ORGANISM Ustilago maydis
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
REFERENCE 1 (bases 1 to 39)
AUTHORS Nugent, K.G., Choffe, K. and Saville, B.J.
TITLE Gene expression during Ustilago maydis diploid filamentous growth:
EST library creation and analyses
JOURNAL Fungal Genet. Biol. 41 (3), 349-360 (2004)
PUBMED 14761795
COMMENT Contact: Barry J. Saville
Saville Lab
University of Toronto
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Fax: 905 828 3792
Email: bsaville@utoronto.ca
Plate: UTM-UM-D126/7-047-UTM row: 04 column: H
Seq primer: T7 Reverse (5' GAGTATACGACTCTACTATAGG 3')
High quality sequence stop: 39.
FEATURES
source
location/Qualifiers
1..39
/organism="Ustilago maydis"
/mol_type="mRNA"
/strain="PBD12"
/db_xref="taxon:5270"
/cell_type="Mycelia"
/dev_stage="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"
/note=Vector: pSport; mRNA was extracted from diploid
mycelia. A cDNA library was constructed and
unidirectionally cloned into pSPORT plasmid, with the use
of the Superscript II cDNA Library Construction Kit."
ORIGIN
Query Match 68.9%; Score 12.4; DB 6; Length 39;
Best Local Similarity 92.9%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 TCTAGAACTGCCCA 17
Db 33 TCTAGAACTACCCA 20
RESULT 12
LOCUS CD967875
DEFINITION SEV 37 Genetag2 Zea mays cDNA, mRNA sequence.
ACCESSION CD967875
VERSION CD967875.1 GI:32828197
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 65)
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Unpublished (2003)
JOURNAL Unpublished
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
location/Qualifiers
1..65
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="mixture"
/db_xref="taxon:4577"
/clone_lib="Genetag2"
ORIGIN
Query Match 68.9%; Score 12.4; DB 6; Length 65;
Best Local Similarity 92.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CTCTCTAGAACTGC 14
Db 35 CTCTCGAGAACTGC 48
RESULT 13
LOCUS CR136088/c
DEFINITION CR136088 80 bp DNA linear GSS 06-JUL-2004
Reverse strand read from insert in 3'HPRT insertion targeting and
chromosome engineering clone MHP358e14, genomic survey sequence.
ACCESSION CR136088
VERSION CR136088.1 GI:49883814
KEYWORDS GSS; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 80)
AUTHORS Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J. and Bradley, A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES
source
location/Qualifiers
1..80
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHP358e14"
/clone_lib="MHP3"
ORIGIN
Query Match 68.9%; Score 12.4; DB 11; Length 80;
Best Local Similarity 92.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 TCTAGAACTGCCCA 17
Db 27 TCTATACTGCCCA 14
RESULT 14
LOCUS BZ594304/c
DEFINITION BZ594304 67 bp DNA linear GSS 07-JAN-2003
SALK_083788.31.75.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_083788.31.75.x, genomic
survey sequence.
ACCESSION BZ594304
VERSION BZ594304.1 GI:27534823
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
```


REFERENCE 1 (bases 1 to 67)
 AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
 Gadrinab,C., Jesse,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 Shinn,P., Zimmerman,J. and Ecker,J.R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.
 FEATURES Location/Qualifiers
 source 1..67
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK 083788.31.75.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /notes="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"
 ORIGIN
 Query Match 67.8%; Score 12.2; DB 9; Length 67;
 Best Local Similarity 82.4%; Pred. No. 1.5e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CTGCTAGAACTGCCCA 17
 |||||
 Db 37 CTGTTTAAACTGCCCA 21
 RESULT 15
 AAl18970/c
 LOCUS AAl18970.1 70 bp mRNA linear EST 17-FEB-1997
 DEFINITION mp61h08.r1 Soares thymus 2NDMT Mus musculus cDNA clone IMAGE:573759
 5' similar to TR:G1166576 G1166576 170 KDA SYNAPTOTANIN ISOFORM ;,
 mRNA sequence.
 ACCESSION AAl18970
 VERSION AAl18970.1 GI:11676514
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 70)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Stepcoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mousees@watson.wustl.edu
 This clone is available royalty-free through LBNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:348407
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 1.
 FEATURES Location/Qualifiers
 source 1..70
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:573759"
 /sex="male"
 /tissue_type="Thymus"
 /dev_stage="4 weeks"
 /lab_host="DH10B"
 /clone_lib="Soares thymus 2NBMT"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not 1 - oligo(dT) primer [5'
 TGTATCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTTTTTT
 3']; double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not 1 and cloned into the Not 1
 and Eco RI sites of the modified pT7T3 vector. RNA
 provided by Dr. Bertrand Jordan. Library went through two
 rounds of normalization, and was constructed by Bento
 Soares and M.Fatima Bonaudo."
 ORIGIN
 Query Match 67.8%; Score 12.2; DB 1; Length 70;
 Best Local Similarity 82.4%; Pred. No. 1.5e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CTGCTAGAACTGCCCA 17
 |||||
 Db 19 CTTTCGAGAACTGCCCA 3
 RESULT 16
 LOCUS CL639237
 DEFINITION CL639237 72 bp mRNA linear GSS 22-MAR-2005
 G084C11 GUTC Gene Trap Library GV07C05 Mus musculus cDNA clone
 G084C11, mRNA sequence.
 ACCESSION CL639237
 VERSION CL639237.2 GI:61684937
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 72)
 AUTHORS Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F.,
 Arnold,H.H., Schutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P.
 TITLE A large-scale, gene-driven mutagenesis approach for the functional
 analysis of the mouse genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
 PUBMED 12904583
 COMMENT On Mar 22, 2005 this sequence version replaced gi:49487684.
 Contact: GUTC
 German Genetrap Consortium (GUTC)
 Email: info@genetrap.de
 U3CEO gene trap. Sequence tag generated by 5' RACE. Additional
 sequence information can be found at:
 'http://genetrap.gsf.de/project/web_new/database/result_clone.html?
 clone_id=G084C11'. ES cell line harboring insertion mutation of
 target gene is available at:
 'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
 1'. Inhouse Sequence Identifier: 23498
 Class: Gene Trap.
 FEATURES Location/Qualifiers
 source 1..72
 /organism="Mus musculus"

```

/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="G084C11"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells (C57BL/6J x 129Sv/SvEvTac) F1"
/clone_lib="GTC Gene Trap Library GV07C05"
/note="Vector: U3CEO"

ORIGIN
Query Match      67.8%; Score 12.2; DB 10; Length 72;
Best Local Similarity 82.4%; Pred. No. 1.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCCA 17
    ||| ||| ||| ||| |||
Db 18 CTGGCGAGAACTGGCCA 34

RESULT 17
A1941463
LOCUS      A1941463      73 bp      mRNA      linear      EST 12-JUL-2004
DEFINITION      sb90c02.y1 Gm-cl017 Glycine max cDNA clone GENEOME SYSTEMS CLONE ID:
                  Gm-cl017-699 5' similar to TR:Q39154 Q39154 MYB-RELATED PROTEIN. ; ,
                  mRNA sequence.
ACCESSION      A1941463
VERSION        A1941463.1 GI:5688448
KEYWORDS       EST.
SOURCE         Glycine max (soybean)
ORGANISM       Glycine max
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                Glycine.
REFERENCE      1 (bases 1 to 73)
AUTHORS       Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Corvett,V.,
                Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
                Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
                Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
                Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
                McCann,R., Waterston,R. and Wilson,R.
TITLE         Public Soybean EST Project
JOURNAL       Unpublished (1999)
COMMENT       Contact: Shoemaker R/Public Soybean EST Project
                Public Soybean EST Project
                Washington University School of Medicine
                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                Tel: 314 286 1800
                Fax: 314 286 1810
                Email: est@watson.wustl.edu
                When it has been determined, an EST from the other end of this
                clone is listed in the 'Other ESTs on clone' field. Trace
                considered overall poor quality Possible reversed clone: similarity
                on wrong strand This clone is available through: Biogenetic
                Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423
                4163; email: info@biogeneticservices.com)
                High quality sequence stop: 1.
                Location/Qualifiers
FEATURES       source
                1..73
                /organism="Glycine max"
                /mol_type="mRNA"
                /cultivar="Williams 82"
                /db_xref="taxon:3847"
                /clone="GENOME SYSTEMS CLONE ID: Gm-cl017-699"
                /tissue_type="vegetable buds of field grown plants"
                /lab_host="XL10-Gold"
                /clone_lib="Gm-cl017"
                /note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
                XhoI; This cDNA library was constructed from mRNA isolated
                from vegetable buds of field grown plants. The cDNA
                library was prepared using the Stratagene pBluescript II
                XR library construction kit. Complementary DNA was

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synthesized from mRNA using a primer consisting of a poly
(dt) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into XL10-Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
Erpelting."

ORIGIN
Query Match      67.8%; Score 12.2; DB 1; Length 73;
Best Local Similarity 82.4%; Pred. No. 1.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGTCTAGAACTGCCAG 18
    ||| ||| ||| ||| |||
Db 42 TGCTAGAACTGGCAAG 58

RESULT 18
AL850449
LOCUS      AL850449      73 bp      mRNA      linear      EST 26-NOV-2003
DEFINITION      AL850449 XGC-egg Xenopus tropicalis cDNA clone TEG9009110 5', mRNA
                  sequence.
ACCESSION      AL850449
VERSION        AL850449.2 GI:38561596
KEYWORDS       EST.
SOURCE         Xenopus tropicalis (western clawed frog)
ORGANISM       Xenopus tropicalis
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
                Xenopodinae; Xenopus; Silurana.
REFERENCE      1 (bases 1 to 73)
AUTHORS       Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE         Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL       Unpublished (2003)
COMMENT       On Sep 15, 2002 this sequence version replaced gi:22870671.
                Contact: Taylor R
                Sanger Institute
                Hinxton, Cambridgeshire, CB10 1SA, UK
                Email: trop@sanger.ac.uk
                Sanger Xenopus tropicalis EST project 2001
                TROPICALIS_SEQUENCE ID: TEG9009110.pkSP6
                Sequencing primer: SP6
                This sequence is from a Xenopus Gene Collection (XGC) library
                constructed by Aaron M. Zorn.
                cDNA was oligo dt primed from Sug of poly A+ RNA from egg.
                EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
                5' end and NotI at the 3' end.
                Vector: pCS107; Site 1: EcoRI; Site 2: NotI
                Host: Escherichia coli XL1-Blue.
                Location/Qualifiers
FEATURES       source
                1..73
                /organism="Xenopus tropicalis"
                /mol_type="mRNA"
                /db_xref="taxon:8364"
                /clone="TEG9009110"
                /dev_stage="egg"
                /lab_host="Escherichia coli XL1-blue"
                /clone_lib="XGC-egg"
                /note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
                was oligo dt primed from Sug of poly A+ RNA from egg.
                EcoRI-NotI cut cDNA was then ligated into pCS107 with
                EcoRI at the 5' end and NotI at the 3' end"

ORIGIN
Query Match      67.8%; Score 12.2; DB 1; Length 73;
Best Local Similarity 82.4%; Pred. No. 1.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTGCTAGAACTGCCCA 17
    ||| ||| ||| ||| |||

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Db      24  CTGTTTATAACTGCCTA 40

RESULT 19
CK725727/c
LOCUS   73 bp  mRNA  linear  EST 17-FEB-2004
DEFINITION
Wucheria bancrofti L3 cDNA (SAW96MLW-WBL3)
Wucheria bancrofti cDNA clone SWBBL3CAW03G08 5', mRNA sequence.
ACCESSION
CK725727
VERSION  1
KEYWORDS
SOURCE   CK725727.1 GI:42579265
          EST.
          Wucheria bancrofti
          Wucheria bancrofti
          Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
          Onchocercidae; Wucheria.
          Williams, S.A.
          Genes Expressed in L3 infective stage larvae of Wucheria
          bancrofti
          Unpublished (1999)
          Contact: Steven A. Williams
          Molecular Parasitology
          Smith College Department of Biological Sciences
          Department of Biological Sciences Clark Science Center, Smith
          College, Northampton, MA, 01063, USA
          Tel: 4135853826
          Fax: 4135853786
          Email: genome@smith.edu
          Seq primer: pBluescript SK.
          Location/Qualifiers
            1..73
              /organism="Wucheria bancrofti"
              /mol_type="mRNA"
              /db_xref="taxon:6293"
              /clone="SWBBL3CAW03G08"
              /dev_stage="L3 infective stage larvae"
              /lab_host="XLI-Blue MRP"
              /note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:
              Xho I; Lymphatic filarial nematode parasite of humans.
              mRNA was prepared from approximately 8,000 L3 isolated
              from mosquitoes in Cairo, Egypt and converted to
              double-stranded cDNA using reverse transcriptase and
              oligo(dT) followed by RNase H and DNA pol I. The library
              has 1.0 x 106 independent recombinants and the average
              insert size is ~900 bp. The library was constructed by
              Michelle Lizotte-Waniewski. The library is available
              from Dr.S.A.Williams, email: genome@smith.edu."

ORIGIN
Query Match      67.8%; Score 12.2; DB 7; Length 73;
Best Local Similarity 82.4%; Pred. No. 1.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2  TGTCTAGAACTGCCAC 18
      |||||
Db   51  TGTCTATAAATGTCCAG 35

RESULT 20
AZ663994/c
LOCUS   73 bp  DNA  linear  GSS 14-DEC-2000
DEFINITION
1M0543M20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0543M20 R, genomic survey sequence.
ACCESSION
AZ663994
VERSION  1
KEYWORDS
SOURCE   AZ663994.1 GI:11801140
          GSS.
          Mus musculus (house mouse)
          Mus musculus
          ORGANISM
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muridae; Murinae; Mus.
          1 (bases 1 to 73)

REFERENCE
1 (bases 1 to 73)

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0543 row: M column: 20
Seq primer: CACACAGGNAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 73.
Location/Qualifiers
  1..73
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0543M20"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptor DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptor mouse DNA was annealed to
    adaptor vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."

ORIGIN
Query Match      67.8%; Score 12.2; DB 9; Length 73;
Best Local Similarity 82.4%; Pred. No. 1.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2  TGTCTAGAACTGCCAC 18
      |||||
Db   48  TATGTAGCACTGCCAC 32

RESULT 21
BG749927/c
LOCUS   78 bp  mRNA  linear  EST 15-MAY-2001
DEFINITION
602708668F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:484352 5',
mRNA sequence.
ACCESSION
BG749927
VERSION  1
KEYWORDS
SOURCE   BG749927.1 GI:14060580
          EST.
          Homo sapiens (human)
          Homo sapiens
          ORGANISM
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.

```

REFERENCE 1 (bases 1 to 78)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: L1CM1684 row: g column: 17
 High quality sequence stop: 78.

FEATURES

source

1. .78
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4845352"
 /tissue_type="normal pigmented retinal epithelium"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 43"
 /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library. |"

ORIGIN

Query Match 67.8%; Score 12.2; DB 2; Length 78;
 Best Local Similarity 82.4%; Pred. No. 1.6e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGCTAGAACTGCCAG 18

||||| ||||| |||||

Db 32 TGCTGGAGTGCACAG 16

RESULT 22

AZ663149
 LOCUS AZ663149 78 bp DNA linear GSS 14-DEC-2000
 DEFINITION 1M0542E07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0542E07 R, genomic survey sequence.

ACCESSION AZ663149.1 GI:11800295

VERSION GSS.

KEYWORDS Mus musculus (house mouse)

SOURCE

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 78)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0542 row: E column: 07
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 78.

FEATURES

source

1. .78
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0542E07"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (GI:4732114|GB|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 67.8%; Score 12.2; DB 9; Length 78;
 Best Local Similarity 82.4%; Pred. No. 1.6e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGCTAGAACTGCCAG 18

||||| ||||| |||||

Db 28 TGCTATTACTGCTAG 44

RESULT 23

BG868495/c

LOCUS

DEFINITION

mRNA sequence.

ACCESSION

BG868495

VERSION

BG868495.1

KEYWORDS

EST.

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 80)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10814 row: p column: 19

High quality sequence stop: 52.

Location/Qualifiers

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/mol_type="mRNA"
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/clone_lib="NCI_CGAP_SG2"
/notes="Organ: salivary gland; Vector: pCMV-SPORT6; Site 1:
NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match      67.8%; Score 12.2; DB 2; Length 80;
Best Local Similarity 82.4%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1 CTGCTAGAACTGCCCA 17
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Db   46 CTGGCTAGAACACCCCA 30

RESULT 24
BH608861
LOCUS      76 bp      DNA      linear      GSS 11-AUG-2003
DEFINITION 15f21 LL18NC02-trapped exons Homo sapiens genomic clone 15f21,
genomic survey sequence.
ACCESSION  BH608861
VERSION     BH608861.1 GI:27437317
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 76)
AUTHORS     Chen,H., Wang,N., Huo,Y., Sklar,P., MacKinnon,D.F., Potash,J.B.,
McMahon,F.J., Antonarakis,S.E., DePaulo,J.R. Jr, Ross,C.A. and
McInnis,M.G.
TITLE       Trapping and sequence analysis of 1138 putative exons from human
chromosome 18
JOURNAL     Mol. Psychiatry 8 (6), 619-623 (2003)
PUBMED     12851638
COMMENT     Contact: Haiming Chen
            Department of Psychiatry
            Johns Hopkins University School of Medicine
            600 N. Wolfe Street, MD 21287-7463, USA
            Tel: 410 614 1530
            Fax: 410 614 4728
            Email: hc@jhmi.edu
            Class: exon-trapped.

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 CTGCTAGAACT 12
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Db   5 CTGCTAGAACT 16

RESULT 25
BJ034925/c
LOCUS      77 bp      mRNA      linear      EST 26-SEP-2003

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DEFINITION  BJ034925 NIBB Mochii normalized Xenopus neurula library Xenopus
laevis cDNA clone XL031f09 5', mRNA sequence.
ACCESSION  BJ034925
VERSION     BJ034925.1 GI:17396669
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
ORGANISM    Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE   1 (bases 1 to 77)
AUTHORS     Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
            Kohara,I.
TITLE       Expressed genes in X. laevis embryo
JOURNAL     Unpublished (2001)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp
            The information of this clone is available through the following
            URL.
            http://xenopus.nibb.ac.jp.

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ORIGIN

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 TCTAGAACTGCC 15
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Db   20 TCTAGAACTGCC 9

Search completed: March 3, 2006, 11:01:29
Job time : 999.737 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:16:16 ; Search time 376.932 Seconds
(without alignments)
2714.499 Million cell updates/sec

Title: US-10-655-801-21

Perfect score: 18

Sequence: 1 tgccctgagaacttcggg 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5881141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2389942

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

GenEmbl:

1: gb_da.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_vt.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	13.8	76.7	20	6	AR366674 Sequence
C 2	13.2	73.3	29	6	E07880 PCR primer
C 3	13.2	73.3	51	6	Q002237 Sequence
C 4	13.2	73.3	51	6	AR444282 Sequence
C 5	13.2	73.3	51	6	AR444283 Sequence
C 6	13.2	73.3	65	6	Q055558 Sequence
C 7	13.2	73.3	69	8	AF189371 Homo sapi
C 8	13	72.2	65	6	Q0554821 Sequence
C 9	12.8	71.1	24	6	AX447262 Sequence
C 10	12.4	68.9	22	6	AR492436 Sequence
C 11	12.4	68.9	31	6	AX249088 Sequence
C 12	12.4	68.9	32	6	AR104789 Sequence
C 13	12.4	68.9	38	6	AX220481 Sequence
C 14	12.4	68.9	38	6	AX425282 Sequence
C 15	12.4	68.9	39	6	I34472 Sequence
C 16	12.4	68.9	60	6	Q0538517 Sequence
C 17	12.4	68.9	60	6	Q0542067 Sequence
C 18	12.4	68.9	60	6	Q0547296 Sequence

19	12.4	68.9	68	6	I13480
C 20	12.4	68.9	80	6	BD074975 Microbial
C 21	12.4	68.9	80	6	AR210850 Sequence
C 22	12.4	68.9	80	6	AR428218 Sequence
C 23	12.2	67.8	20	6	AR584458 Sequence
C 24	12.2	67.8	27	6	AX813491 Sequence
C 25	12.2	67.8	28	6	BD237704 Therapeut
C 26	12.2	67.8	28	6	AX278222 Sequence
C 27	12.2	67.8	36	6	AR060746 Sequence
C 28	12.2	67.8	36	6	AX611150 Sequence
C 29	12.2	67.8	36	6	AR393439 Sequence
C 30	12.2	67.8	51	6	AX115865 Sequence
C 31	12.2	67.8	51	6	AX199214 Sequence
C 32	12.2	67.8	60	6	CQ542005 Sequence
C 33	12.2	67.8	60	6	CQ544069 Sequence
C 34	12.2	67.8	60	6	CQ548009 Sequence
C 35	12.2	67.8	60	6	CQ561846 Sequence
C 36	12.2	67.8	60	6	AR393440 Sequence
C 37	12.2	67.8	65	6	CQ556854 Sequence
C 38	12.2	67.8	65	6	CQ558504 Sequence
C 39	12	66.7	20	6	AR649203 Sequence
C 40	12	66.7	36	6	AR337977 Sequence
C 41	12	66.7	38	6	AR336109 Sequence
C 42	12	66.7	51	6	CQ004183 Sequence
C 43	12	66.7	61	6	CQ919690 Sequence
C 44	11.8	65.6	17	6	BD199011 Method an
C 45	11.8	65.6	17	6	BD199012 Method an
C 46	11.8	65.6	18	6	E63218 NAIP transg
C 47	11.8	65.6	19	6	AX840264 Sequence
C 48	11.8	65.6	20	6	A01587 Oligonucleo
C 49	11.8	65.6	20	6	A03836 Nucleotide
C 50	11.8	65.6	20	6	A10446 Synthetic n
C 51	11.8	65.6	20	6	A78920 Sequence 18
C 52	11.8	65.6	20	6	BD190250 Method fo
C 53	11.8	65.6	20	6	I27212 Sequence 18
C 54	11.8	65.6	20	6	I63095 Sequence 18
C 55	11.8	65.6	20	6	AR312197 Sequence
C 56	11.8	65.6	20	6	AX662813 Sequence
C 57	11.8	65.6	21	6	AR528869 Sequence
C 58	11.8	65.6	21	6	AX094894 Sequence
C 59	11.8	65.6	24	6	AR156602 Sequence
C 60	11.8	65.6	24	6	BD221710 Process f
C 61	11.8	65.6	24	6	BD261665 Method of
C 62	11.8	65.6	24	6	AR216734 Sequence
C 63	11.8	65.6	24	6	AR473813 Sequence
C 64	11.8	65.6	24	6	AR482295 Sequence
C 65	11.8	65.6	25	6	A45599 Sequence 4
C 66	11.8	65.6	25	6	AR082280 Sequence
C 67	11.8	65.6	25	6	AR082303 Sequence
C 68	11.8	65.6	25	6	AR120822 Sequence
C 69	11.8	65.6	25	6	AR120845 Sequence
C 70	11.8	65.6	25	6	CQ876140 Sequence
C 71	11.8	65.6	25	6	I12721 Sequence 19
C 72	11.8	65.6	25	6	I12722 Sequence 20
C 73	11.8	65.6	25	6	I78326 Sequence 12
C 74	11.8	65.6	25	6	I78349 Sequence 14
C 75	11.8	65.6	25	6	BD022730 Mammary c
C 76	11.8	65.6	27	6	A22395 primer DNA
C 77	11.8	65.6	27	6	AR146226 Sequence
C 78	11.8	65.6	27	6	AX067186 Sequence
C 79	11.8	65.6	29	6	A44164 Sequence 7
C 80	11.8	65.6	29	6	BD192229 Secreted
C 81	11.8	65.6	30	6	CQ972003 Sequence
C 82	11.8	65.6	30	6	E32668 Peptide inh
C 83	11.8	65.6	30	6	E32673 Peptide inh
C 84	11.8	65.6	31	6	CQ877214 Sequence
C 85	11.8	65.6	34	6	A58326 Sequence 4
C 86	11.8	65.6	34	6	A92326 Sequence 6
C 87	11.8	65.6	34	6	AR105324 Sequence
C 88	11.8	65.6	34	6	AX337942 Sequence
C 89	11.8	65.6	34	6	BD009958 Retrovira
C 90	11.8	65.6	36	6	A58325 Sequence 3
C 91	11.8	65.6	36	6	A63212 Sequence 10

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92 11.8 65.6 36 6 A92325 Sequence 5
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96 11.8 65.6 36 6 AR257264 Sequence
97 11.8 65.6 36 6 AR590072 Sequence
98 11.8 65.6 36 6 AR592969 Sequence
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ALIGNMENTS

RESULT 1
AR366674/c
LOCUS AR366674 20 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 36 from patent US 6329203.
ACCESSION AR366674
VERSION AR366674.1 GI:34599266
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.F. and Wyatt,J.
TITLE Antisense modulation of glioma-associated oncogene-1 expression
JOURNAL Patent: US 6329203-A 36 11-DEC-2001;
ISIS Pharmaceuticals, Inc.; Carlsbad, CA
FEATURES
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Best Local Similarity 88.2%; Pred. No. 3.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCCTTGAGAACTTCGGG 18
Db 18 GCCTTGAGAACTTCAGG 2

RESULT 2
E07880/c
LOCUS E07880 29 bp DNA linear PAT 29-SEP-1997
DEFINITION PCR primer for gaining part of surface antigen protein of Japanese
encephalitis virus.
ACCESSION E07880
VERSION E07880.1 GI:2176012
KEYWORDS JP 1994205672-A/2.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 29)
AUTHORS Sato,T., Takamura,C., Yasuda,A., Kamogawa,K. and Yasui,K.
TITLE PRODUCTION OF CHIMERAL PROTEIN HAVING ANTIGEN SITE OF SURFACE
ANTIGEN PROTEIN OF JAPANESE ENCEPHALITIS VIRUS AND HEPATITIS B
VIRUS AND RECOMBINANT BACULOVIRUS THEREFOR
JOURNAL Patent: JP 1994205672-A 2 26-JUL-1994;
NIPPON ZEON CO LTD, TOKYO MET GOV SHINKEI KAGAKU SOGO KENKYUSHO
COMMENT OS None
OC Artificial sequences.
PN JP 1994205672-A/2
PD 26-JUL-1994
PF 19-NAR-1992 JP 1992063699
PI SATO TAKANORI, TAKAMURA CHIZUKO, YASUDA ATSUSHI, PI KAMOGAWA KOICHI,
PI YASUI KOTARO
PC C12N7/01,A61K39/155,A61K39/29,A61K39/295,C12N15/62,C12N15/86,
PC C12P21/02,
PC (C12N15/62,C12R1.92),(C12P21/02,C12R1.91);

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CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No; Location/Qualifiers
FH Key
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 18 TGCCTTGAGAACTTCGAG 1

RESULT 3
CQ002237
LOCUS CQ002237 51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 877 from Patent WO0147944.
ACCESSION CQ002237
VERSION CQ002237.1 GI:41008869
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0147944-A 877 05-JUL-2001;
Curagen Corporation (US)
FEATURES
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1..51
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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ORIGIN
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Best Local Similarity 83.3%; Pred. No. 7.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTTCGGG 18
Db 25 TGCCTCAGAACTTCGGG 42

RESULT 4
AR444282
LOCUS AR444282 51 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 693 from patent US 6670464.
ACCESSION AR444282
VERSION AR444282.1 GI:42672061
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.

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TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

JOURNAL Patent: US 6670464-A 693 30-DEC-2003;
Curagen Corporation; New Haven, CT

FEATURES
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ORIGIN

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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18
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Db 33 TGCCTTGAGAACTTCGGG 50

RESULT 5
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LOCUS Sequence 694 from patent US 6670464.
DEFINITION AR444283
ACCESSION AR444283
VERSION AR444283.1 GI:42672062
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkete,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: US 6670464-A 694 30-DEC-2003;
Curagen Corporation; New Haven, CT

FEATURES
source
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ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 51;
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 6
CQ555558
LOCUS Sequence 25193 from Patent WO0210449.
DEFINITION CQ555558
ACCESSION CQ555558
VERSION CQ555558.1 GI:41521985
KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 25193 07-FEB-2002;
Compugen Inc. (US)

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ORIGIN

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Best Local Similarity 83.3%; Pred. No. 7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18
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Db 3 TGCCTTGAGAACTTCGGG 20

RESULT 7

AF189371
LOCUS Homo sapiens clone B31U T-cell receptor beta chain (TCRBV20S1)
DEFINITION AF189371
ACCESSION AF189371
VERSION AF189371.1 GI:6841609
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
REFERENCE 1 (bases 1 to 69)
AUTHORS Soudeyns,H., Champagne,P., Holloway,C.L., Silvestri,G.U.,
Ringuette,N., Samson,J., Lapointe,N. and Sekaly,R.P.
TITLE Transient T cell receptor beta-chain variable region-specific expansions of CD4+ and CD8+ T cells during the early phase of pediatric human immunodeficiency virus infection: characterization of expanded cell populations by T cell receptor phenotyping
JOURNAL J. Infect. Dis. 181 (1), 107-120 (2000)
PUBMED 10608757
REFERENCE 2 (bases 1 to 69)
AUTHORS Soudeyns,H., Champagne,P., Holloway,C.L., Silvestri,G.U.,
Ringuette,N., Samson,J., Lapointe,N. and Sekaly,R.P.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-1999) Laboratoire d'immunologie, IRCM, 110 avenue
Des Pins ouest, Montreal, Quebec H2W 1R7, Canada

FEATURES

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/translation="LLSDSGFYLCAMSTSGRTYEYF"

ORIGIN

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Best Local Similarity 83.3%; Pred. No. 7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18
||||| ||||| ||||| |||||
Db 30 TGCCTTGAGAACTTCAGG 47

RESULT 8

CQ554821
LOCUS Sequence 24456 from Patent WO0210449.
DEFINITION CQ554821
ACCESSION CQ554821
VERSION CQ554821.1 GI:41521248
KEYWORDS

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
AUTHORS Oligonucleotide library for detecting rna transcripts and splice
TITLE variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 24456 07-FEB-2002;
CompuGen Inc. (US)
FEATURES Location/Qualifiers
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/db_xref="taxon:10090"
ORIGIN
Query Match 72.2%; Score 13; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 TGAGAACTTCGG 18
|||||
Db 10 TGAGAACTTCGG 22
RESULT 9
AX447262/c
LOCUS AX447262 24 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 3717 from Patent WO0216649.
ACCESSION AX447262
VERSION AX447262.1 GI:21696161
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Gunderson,K.
TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 3717 28-FEB-2002;
Illumina, Inc. (US)
FEATURES Location/Qualifiers
source 1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."
ORIGIN
Query Match 71.1%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 TGCCTTGAGAACTTCG 16
|||||
Db 23 TGCTTAGATCTTCG 8
RESULT 10
AR492436
LOCUS AR492436 22 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 5 from patent US 6716813.
ACCESSION AR492436
VERSION AR492436.1 GI:47261588
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Lim,D.J., Lee,H.-Y., Webster,P., Andalibi,A., Li,J.-D. and Ganz,T.
TITLE Use of antimicrobial proteins and peptides for the treatment of
otitis media and paranasal sinusitis

JOURNAL Patent: US 6716813-A 5 06-APR-2004;
House Ear Institute; Los Angeles, CA
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
/mol_type="genomic DNA"
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Query Match 68.9%; Score 12.4; DB 6; Length 22;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GCCTTGAGAACTTC 15
|||||
Db 2 GCCATGAGAACTTC 15
RESULT 11
AX249088/c
LOCUS AX249088 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 1167 from Patent WO0166800.
ACCESSION AX249088
VERSION AX249088.1 GI:15863711
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 1167 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES Location/Qualifiers
source 1..31
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 68.9%; Score 12.4; DB 6; Length 31;
Best Local Similarity 81.2%; Pred. No. 2e+05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 2 GCCTTGAGAACTTCG 17
|||||
Db 29 GTCTTGAGAACTTYG 14
RESULT 12
AR104789/c
LOCUS AR104789 32 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 86 from patent US 6093811.
ACCESSION AR104789
VERSION AR104789.1 GI:12817497
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Bennett,C.Frank. and Mirabelli,C.K.
TITLE Oligonucleotide modulation of cell adhesion
JOURNAL Patent: US 6093811-A 86 25-JUL-2000;
FEATURES Location/Qualifiers
source 1..32
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 68.9%; Score 12.4; DB 6; Length 32;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 4 CTTGAGAACTCGG 17
Db 31 CTTGAGAACTTCAG 18

RESULT 13
AX220481/c
LOCUS AX220481 38 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 5923 from Patent WO0159103.
ACCESSION AX220481
VERSION AX220481.1 GI:15548205
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source 1..38
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/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN
Query Match 68.9%; Score 12.4; DB 6; Length 38;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTT 14
Db 37 TGCCTTGAGAACTT 24

RESULT 14
AX425282/c
LOCUS AX425282 38 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 3618 from Patent WO0188124.
ACCESSION AX425282
VERSION AX425282.1 GI:21528664
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., McLaughlin, F.G. and
Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source 1..38
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

ORIGIN
Query Match 68.9%; Score 12.4; DB 6; Length 38;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTT 14
Db 37 TGCCTTGAGAACTT 24

RESULT 15
I34472
LOCUS I34472 39 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 11 from patent US 5597908.
ACCESSION I34472
VERSION I34472.1 GI:1825263
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 39)
AUTHORS Taddei-Peters, W.C. and Butler, S.M.
TITLE Immunoreactive peptides of apo(a)
JOURNAL Patent: US 5597908-A 11 28-JAN-1997;
FEATURES
source 1..39
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/mol_type="unassigned DNA"

ORIGIN
Query Match 68.9%; Score 12.4; DB 6; Length 39;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCCTTGAGAACTTC 15
Db 25 GCCTTGAGAACTTC 12

RESULT 16
CQ538517
LOCUS CQ538517 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 8152 from Patent WO0210449.
ACCESSION CQ538517
VERSION CQ538517.1 GI:41504781
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 8152 07-FEB-2002;
Compugen Inc. (US)
FEATURES
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/db_xref="taxon:9606"

ORIGIN
Query Match 68.9%; Score 12.4; DB 6; Length 60;
Best Local Similarity 92.9%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TTGAGAACTTCGG 18
Db 29 TTGAGAACTTCGG 42

RESULT 17
CQ542067
LOCUS CQ542067 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 11702 from Patent WO0210449.
ACCESSION CQ542067
VERSION CQ542067.1 GI:41508331
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 8152 07-FEB-2002;
Compugen Inc. (US)
FEATURES
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/db_xref="taxon:9606"

ORIGIN
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Best Local Similarity 92.9%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TTGAGAACTTCGG 18
Db 29 TTGAGAACTTCGG 42

RESULT 17
CQ542067
LOCUS CQ542067 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 11702 from Patent WO0210449.
ACCESSION CQ542067
VERSION CQ542067.1 GI:41508331
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 8152 07-FEB-2002;
Compugen Inc. (US)
FEATURES
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/db_xref="taxon:9606"

ORIGIN
Query Match 68.9%; Score 12.4; DB 6; Length 60;
Best Local Similarity 92.9%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TTGAGAACTTCGG 18
Db 29 TTGAGAACTTCGG 42

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 11702 07-FEB-2002;
CompuGen Inc. (US)

FEATURES
source Location/Qualifiers
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ORIGIN

Query Match 68.9%; Score 12.4; DB 6; Length 60;
Best Local Similarity 92.9%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCTTGAGAACTTCG 16
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Db 25 CCTTGAGAACTTCG 38
|||||

RESULT 18
CQ547296 60 bp DNA linear PAT 30-JAN-2004
LOCUS
DEFINITION Sequence 16931 from Patent WO0210449.
ACCESSION CQ547296
VERSION CQ547296.1 GI:41513560
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 16931 07-FEB-2002;
CompuGen Inc. (US)

FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCCTTGAGAACTTC 15
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Db 3 GCCTTGAGAACTTC 16
|||||

RESULT 19
I13480 68 bp DNA linear PAT 26-JUL-1995
LOCUS
DEFINITION Sequence 14 from patent US 5436391.
ACCESSION I13480
VERSION I13480.1 GI:910821
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE
AUTHORS Fujimoto,H., Ito,K., Yamamoto,M. and Shimamoto,K.
TITLE Synthetic insecticidal gene, plants of the genus oryza transformed
with the gene, and production thereof
JOURNAL Patent: US 5436391-A 14 25-JUL-1995;

FEATURES
source Location/Qualifiers
1..68
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

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Best Local Similarity 92.9%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCTTGAGAACTTCG 16
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Db 21 CCTTGAGAACTTCG 34
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RESULT 20
BD074975/c 80 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Microbial gene of secreted beta-glucuronidase, gene product, and
utilization thereof.
ACCESSION BD074975
KEYWORDS BD074975.1 GI:22620578
VERSION JP 2001515724-A/51.
SOURCE synthetic construct
ORGANISM other sequences: artificial sequences.

REFERENCE
AUTHORS Jefferson,R.A., Kilian,A. and Keese,P.K.
TITLE Microbial gene of secreted beta-glucuronidase, gene product, and
utilization thereof
JOURNAL Patent: JP 2001515724-A 51 25-SEP-2001;
CAMBIA BIOSYSTEMS LLC

COMMENT
OS Artificial Sequence
FN JP 2001515724-A/51
PD 25-SEP-2001
PF 09-SEP-1998 JP 2000510870
PI 09-SEP-1997 US 60/058263
PI RICHARD A. JEFFERSON, ANDRZEJ KILIAN, PAUL KONRAD KEESE, PC
C12N15/09, A01H5/00, A01K67/027, C12N1/15, C12N1/19, C12N1/21 PC
C12N5/10, C12N5/10,
PC C12N9/24, C12Q1/02, G01N33/52// (C12N15/09, C12R1/07), (C12N15/09,
C12R1/19),
PC (C12Q1/02, C12R1/07), C12N15/00, C12N5/00, C12N5/00, (C12N15/00, PC
C12R1/07),
PC (C12N15/00, C12R1/19)
CC Description of Artificial Sequence: Oligonucleotide. CC
Product of Synthesis to Overlap and create fragments of CC
engineered
CC secrettable microbial GUS (Figure 13)
FH Key Location/Qualifiers
FT source 1..80
FT /organism='Artificial Sequence'.

FEATURES
source Location/Qualifiers
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ORIGIN

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Best Local Similarity 92.9%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TTGAGAACTTCGGG 18
|||||
Db 48 TTGAGAACTTCGTG 35
|||||

RESULT 21
AR210850/c 80 bp DNA linear PAT 20-JUN-2002
LOCUS
DEFINITION Sequence 59 from patent US 6391547.
ACCESSION AR210850

VERSION AR210850.1 GI:21513688
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 80)
 AUTHORS Jefferson, R.A., Harcourt, R. Louise., Kilian, A., Wilson, K. Joanna. and
 TITLE Keese, P. Konrad.
 JOURNAL Microbial .beta.-glucuronidase genes, gene products and uses
 PATENT: US 6391547-A 59 21-MAY-2002;
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 source 1..80
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 Best Local Similarity 92.9%; Pred. No. 1.9e+05;
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 QY 5 TTGAGAACTTCGGG 18
 |||||
 Db 48 TTGAGAACTTCGTG 35
 RESULT 22
 AR428218/c
 LOCUS 80 bp DNA linear PAT 18-DEC-2003
 DEFINITION Sequence 98 from patent US 6641996.
 ACCESSION AR428218
 VERSION AR428218.1 GI:40187611
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 80)
 AUTHORS Jefferson, R.A. and Mayer, J.E.
 TITLE Microbial .beta.-glucuronidase genes, gene products and uses
 JOURNAL thereof
 PATENT: US 6641996-A 98 04-NOV-2003;
 Cambia; ACT;
 AUX;
 FEATURES Location/Qualifiers
 source 1..80
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 /mol_type="genomic DNA"
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 Best Local Similarity 92.9%; Pred. No. 1.9e+05;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 TTGAGAACTTCGGG 18
 |||||
 Db 48 TTGAGAACTTCGTG 35
 RESULT 23
 AR584458
 LOCUS 20 bp DNA linear PAT 15-DEC-2004
 DEFINITION Sequence 57 from patent US 6797475.
 ACCESSION AR584458
 VERSION AR584458.1 GI:56625641
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Barnes, G. and Meyer, J.
 TITLE Detection of polymorphisms in the human 5-lipoxygenase gene
 JOURNAL Patent: US 6797475-A 57 28-SEP-2004;
 Millennium Pharmaceuticals, Inc.; Cambridge, MA

FEATURES Location/Qualifiers
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 /organism="unknown"
 /mol_type="genomic DNA"
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 Query Match 67.8%; Score 12.2; DB 6; Length 20;
 Best Local Similarity 82.4%; Pred. No. 2.6e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 GCCTTGAGAACTTCGGG 18
 |||||
 Db 3 GCACTGAGAACTTCGGG 19
 RESULT 24
 AX813491
 LOCUS 27 bp DNA linear PAT 02-DEC-2003
 DEFINITION Sequence 13 from Patent WO03062276.
 ACCESSION AX813491
 VERSION AX813491.1 GI:38636020
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Ross, R., Artymuk, P. and Savers, J.
 TITLE Multimers of receptor-binding ligands
 JOURNAL Patent: WO 03062276-A 13 31-JUL-2003;
 Asterion Limited (GB)
 FEATURES Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
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 Best Local Similarity 82.4%; Pred. No. 2.6e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TGCCTTGAGAACTTCGG 17
 |||||
 Db 3 TGCCTGAGAACTTCGG 19
 RESULT 25
 BD237704/c
 LOCUS 28 bp DNA linear PAT 17-JUL-2003
 DEFINITION Therapeutically active proteins in plants.
 ACCESSION BD237704
 VERSION BD237704.1 GI:33047474
 KEYWORDS JP 2002526116-A/33.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Heifetz, P.B., Goff, S.A., Tuttle, A.B. and Wenk, M.E.G.
 TITLE Therapeutically active proteins in plants
 JOURNAL Patent: JP 2002526116-A 33 20-AUG-2002;
 SYNGENTA PARTICIPATIONS AG
 COMMENT OS Artificial Sequence
 PN JP 2002526116-A/33
 PD 20-AUG-2002
 PF 05-OCT-1999 JP 2000574707
 PR 07-OCT-1998 US 09/167362, 07-OCT-1998 US 09/168231 PI
 PETER BERNARD HEIFETZ, STEPHEN ARTHUR GOFF, ANNMARIE BLOOM PI
 TUTTLE.
 PI MONIKA ELSE GRIOT WENK
 PC A01H5/00, A23L1/30, A61K38/00, A61K38/15, A61K38/22, PC
 A61K38/28,
 PC A61K38/43, A61K39/00, A61K39/35, A61P29/00, A61P37/00, A61P37/06,
 PC A61P37/08,

PC C12N5/10,C12N15/09/(C12N5/10,C12R1:91),C12N15/00,C12N5/00, PC
 A61K37/02,
 PC A61K37/26,A61K37/48,A61K37/04,A61K37/24,(C12N5/00,C12R1:91) CC
 Description of Artificial Sequence: Oligonucleotide FH Key

Location/Qualifiers
 FT source 1..28

FT Location/Qualifiers
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FEATURES
 source

1..28
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 /mol_type="genomic DNA"
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ORIGIN

Query Match 67.8%; Score 12.2; DB 6; Length 28;
 Best Local Similarity 82.4%; Pred.No. 2.6e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTTCGG 17
 |||||
 Db 26 TTCCTGGAGATCTTCGG 10

Search completed: March 3, 2006, 08:38:52
 Job time : 378.932 secs

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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:02:58 ; Search time 117.534 Seconds
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Title: US-10-655-801-21

Perfect score: 18
Sequence: 1 tgccttgagaacttcggg 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 496997 seqs, 332346308 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	100.0	18	AAH47977	Aah47977 Human ind
2	14.8	82.2	24	ADW47303	Adw47303 Osteopor
3	14	77.8	29	ADW47302	Adw47302 Osteopor
4	13.8	76.7	20	ABK30534	Abk30534 Human gli
5	13.8	76.7	25	ACI93355	Acti93355 Human mic
6	13.4	74.4	30	AAT10512	Aat10512 5' primer
7	13.4	74.4	30	ADO79688	Ado79688 Dpf3 PCR
8	13.4	74.4	30	ADY02087	Ady02087 PCR prime
9	13.2	73.3	20	ADT75569	Adt75569 S. pneumo
10	13.2	73.3	29	AAQ70160	Aaq70160 Primer fo
11	13.2	73.3	51	AAQ77010	Aaq77010 Human clo
12	13.2	73.3	51	AAQ77011	Aaq77011 Human clo
13	13.2	73.3	51	AAQ77012	Aaq77012 Human clo
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15	13.2	73.3	65	ABN52445	Abn52445 Mouse spl
16	13	72.2	21	AAQ79424	Aaq79424 PCR prime
17	13	72.2	50	ADD41511	Add41511 Synthetic
18	13	72.2	63	ADM68520	Adm68520 BtSim rel
19	13	72.2	65	ABN51708	Abn51708 Mouse spl

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21	12.8	71.1	24	6	ABQ03710	Abq03710 Oligonuc1
22	12.8	71.1	36	14	ADY26567	Ady26567 PCR prime
23	12.8	71.1	41	6	ABK88169	Abk88169 Human nuc
24	12.4	68.9	22	8	ABX15037	Abx15037 Human bet
25	12.4	68.9	22	14	ADM12549	Adm12549 Human bet
26	12.4	68.9	25	12	ADP15613	Adp15613 Renal cel
27	12.4	68.9	28	13	ADR72557	Adr72557 Hypoxia-r
28	12.4	68.9	38	4	ABK05923	Abk05923 Human NOG
29	12.4	68.9	38	6	ABK20971	Abk20971 Human ERG
30	12.4	68.9	39	2	AAQ91615	Aaq91615 Human apo
31	12.4	68.9	60	6	ABN44183	Abn44183 Human spl
32	12.4	68.9	60	6	ABN35404	Abn35404 Human spl
33	12.4	68.9	67	8	ABN38954	Abn38954 Human spl
34	12.4	68.9	67	8	ABX92845	Abx92845 C2 domain
35	12.4	68.9	67	12	ADP21643	Adp21643 PCR prime
36	12.4	68.9	80	2	AAQ23815	Aaq23815 Bacillus
37	12.4	68.9	80	3	AAA07919	Aaa07919 Secretabl
38	12.2	67.8	20	6	ABT11169	Abt11169 Human S-1
39	12.2	67.8	20	12	ADO40181	Ado40181 Human MAP
40	12.2	67.8	20	12	ADO40147	Ado40147 Human MAP
41	12.2	67.8	21	10	ADJ81835	Adj81835 Human Na+
42	12.2	67.8	22	8	ADA37146	Ada37146 Human gli
43	12.2	67.8	25	9	ACI11241	Acti11241 Human mic
44	12.2	67.8	25	9	ACI93354	Acti93354 Human mic
45	12.2	67.8	25	9	ACI07700	Acti07700 Human mic
46	12.2	67.8	27	10	ADC06685	Adc06685 PCR prime
47	12.2	67.8	28	3	AAA29801	Aaa29801 Ragweed p
48	12.2	67.8	28	5	AAD21607	Aad21607 Ragweed m
49	12.2	67.8	32	13	ADR49359	Adr49359 C. elegans
50	12.2	67.8	32	13	ADR49359	Adr49359 C. elegans
51	12.2	67.8	36	2	ADT99464	Adt99464 PCR prime
52	12.2	67.8	37	3	AAA38045	Aaa38045 PCR prime
53	12.2	67.8	40	14	ADZ71340	Adz71340 Novel cys
54	12.2	67.8	50	6	ABZ02198	Abz02198 Human leu
55	12.2	67.8	51	4	AAH89363	Aah89363 Human kin
56	12.2	67.8	51	4	AAH38192	Aah38192 Human SNP
57	12.2	67.8	60	6	ABN58733	Abn58733 Human spl
58	12.2	67.8	60	6	ABN38892	Abn38892 Human spl
59	12.2	67.8	60	6	ABN44896	Abn44896 Human spl
60	12.2	67.8	60	6	ABN40956	Abn40956 Human spl
61	12.2	67.8	65	6	ABN55391	Abn55391 Mouse spl
62	12.2	67.8	65	6	ABN53741	Abn53741 Mouse spl
63	12.2	67.8	80	12	ADM95797	Adm95797 Rat antis
64	12	66.7	17	12	ADI81374	Adi81374 HCV DNAB
65	12	66.7	20	6	ABA91933	Abag1933 Coryneb
66	12	66.7	25	9	ACI67569	Acti67569 Human mic
67	12	66.7	36	9	ADB99175	Adb99175 Human PSM
68	12	66.7	36	12	ADJ93247	Adj93247 Human pro
69	12	66.7	36	12	ADN97349	Adn97349 Human C-m
70	12	66.7	51	4	AAQ29615	Aaq29615 Human SNP
71	12	66.7	60	14	ABE46491	Aeb46491 Probe for
72	12	66.7	61	13	ADU10451	Adu10451 Solid tum
73	11.8	65.6	17	2	AAA18811	Aaa18811 Human TIE
74	11.8	65.6	17	2	AAA18812	Aaa18812 Human TIE
75	11.8	65.6	17	13	ADX82734	Adx82734 Mediterra
76	11.8	65.6	17	13	ADX83030	Adx83030 Mediterra
77	11.8	65.6	18	2	AAQ38948	Aaq38948 HIV-1 HXB
78	11.8	65.6	18	4	AAQ171314	Aaq171314 PCR prime
79	11.8	65.6	18	12	ADN48459	Adn48459 Haemoglob
80	11.8	65.6	18	13	ADX83031	Adx83031 Mediterra
81	11.8	65.6	18	13	ADX82735	Adx82735 Mediterra
82	11.8	65.6	19	10	ACF58382	Acf58382 Beta-glob
83	11.8	65.6	19	13	ADX83032	Adx83032 Mediterra
84	11.8	65.6	19	13	ADX82736	Adx82736 Mediterra
85	11.8	65.6	20	2	AAQ93408	Aaq93408 PCR prime
86	11.8	65.6	20	5	ABQ61768	Abq61768 Lentiviru
87	11.8	65.6	20	6	ABQ74654	Abq74654 STEAP gen
88	11.8	65.6	20	8	ABX12662	Abx12662 Non-cycli
89	11.8	65.6	20	10	ADC52099	Adc52099 Caenorhab
90	11.8	65.6	20	12	ADI27596	Adi27596 Human DRA
91	11.8	65.6	20	12	ADI27524	Adi27524 Human DRA
92	11.8	65.6	20	12	ADH80300	Adh80300 STEAP PCR

C 93 11.8 65.6 20 12 ADK80872 Chimeric
 C 94 11.8 65.6 20 12 ADK77211 Chimeric
 C 95 11.8 65.6 20 12 ADK81043 Chimeric
 C 96 11.8 65.6 20 12 ADK76762 Chimeric
 C 97 11.8 65.6 20 12 ADK76861 Chimeric
 C 98 11.8 65.6 20 12 ADK78504 Chimeric
 C 99 11.8 65.6 20 13 ADQ99869 Rice SNP
 C 100 11.8 65.6 20 13 ADR57958 ICER gene

ALIGNMENTS

RESULT 1
 AAH47977
 ID AAH47977 standard; DNA; 18 BP.
 XX AC
 XX AAH47977;
 XX AC
 XX 02-OCT-2001 (first entry)
 XX AC
 XX Human inducible NOS antisense oligonucleotide SEQ ID NO 21.
 XX AC
 XX Antisense oligonucleotide; inducible nitric oxide synthase; NOS;
 KW modulate expression; immunomodulator; antidiabetic; cardiovascular;
 KW cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;
 KW 2'-O-methoxyethyl; phosphorothioate; human; ss.
 XX Homo sapiens.
 XX OS
 XX Key Location/Qualifiers
 FH modified_base 1..18
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone, 5' and 3' four
 FT nucleotide 2'-MOE (2'-O-methoxyethyl) wings (the cytidine
 FT residues in the 2'-MOE wings are 5-methylcytidines) and a
 FT deoxy gap"
 XX
 XX WO200152902-A1.
 XX
 XX 26-JUL-2001.
 XX
 XX 15-JAN-2001; 2001WO-US001381.
 XX
 XX 24-JAN-2000; 2000US-00490208.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Bennett CF, Dean NM, Cowser LM;
 XX WPI; 2001-465340/50.
 XX
 XX New antisense oligonucleotides for modulating the expression of inducible
 PT nitric oxide synthase in cells or tissues, particularly useful for
 PT treating e.g. immunological, cardiovascular or neurological disorders, or
 PT ischemia.

XX Claim 3; Page 83; 144pp; English.

XX The invention relates to antisense compounds, especially
 CC oligonucleotides, which are targeted to a nucleic acid encoding inducible
 CC nitric oxide synthase and which specifically hybridize to and modulate
 CC expression of inducible nitric oxide synthase. The antisense compounds
 CC have immunomodulator, antidiabetic, cardiovascular, cardiant,
 CC neuroprotective, disorder and vasotropic activity. The antisense
 CC oligonucleotides are useful for inhibiting the expression of inducible
 CC nitric oxide synthase in cells or tissues. In particular, the antisense
 CC oligonucleotides are useful for treating diseases or disorders associated
 CC with inducible nitric oxide synthase, e.g. diabetes, immunological
 CC disorder, cardiovascular syndrome, neurological disorder or
 CC ischaemia/reperfusion injury. The antisense oligonucleotides are also
 CC useful for research and diagnostics. The present sequence is that of an

CC antisense 2'-O-methoxyethyl gapmer oligonucleotide with a
 CC phosphorothioate backbone, a central "gap" region of ten nucleotides
 CC flanked by four nucleotide 2'-MOE (2'-methoxyethyl) wings (cytidine
 CC residues in the 2'-MOE wings are 5-methylcytidines) and targeted to human
 CC inducible nitric oxide synthase (NOS) mRNA (AAH47959)
 XX
 SQ Sequence 18 BP; 3 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18
 |||||
 Db 1 TGCCTTGAGAACTTCGGG 18

RESULT 2

ADW47303/C
 ID ADW47303 standard; DNA; 24 BP.
 XX AC
 XX ADW47303;
 XX AC

DT 07-APR-2005 (first entry)

DE Osteoporosis polymorphism detection related primer, SEQ ID 9.

XX SNP detection; osteoporosis; tumor necrosis factor receptor; TNFR;
 KW DNA detection; ss; primer; PCR.

XX Synthetic.

XX JP2005006538-A.

XX 13-JAN-2005.

XX 18-JUN-2003; 2003JP-00173288.

XX 18-JUN-2003; 2003JP-00173288.

XX (UYNI-) UNIV NIPPON IKA.

XX WPI; 2005-114728/13.

XX Detecting polymorphism in genes associated with osteoporosis such as
 PT tumor necrosis factor receptor associated factor binding protein gene,
 PT reverse-inducible LIM domain protein gene and heat shock protein 70 gene.

XX Disclosure; SEQ ID NO 9; 38pp; Japanese.

XX The invention relates to a novel method for detecting polymorphism in
 CC genes associated with osteoporosis, such as a tumor necrosis factor
 CC receptor (TNFR) associated factor binding protein gene, reverse-inducible
 CC LIM domain protein gene, heat shock protein 70 gene, or an alpha-2-
 CC glycoprotein 1 gene. The invention further comprises a kit for
 CC polymorphism gene detection, comprising components for detecting
 CC polymorphism in genes associated with osteoporosis such as TNFR
 CC associated factor binding protein gene, reverse-inducible LIM domain
 CC protein gene, heat shock protein 70 gene, or an alpha-2-glycoprotein 1
 CC gene; a kit for performing an invader assay, comprising components for
 CC detecting polymorphisms chosen from polymorphism at base position 2141,
 CC 1542 or 525 of TNFR associated factor binding protein gene, polymorphism
 CC at base position 6364 in sequence of reverse-inducible LIM domain protein
 CC gene, polymorphism at a base that encodes glutamic acid of position 110
 CC in amino acid sequence of heat shock protein 70 gene, and polymorphism at
 CC base position 1115 in base sequence of alpha-2-glycoprotein 1 gene; and a
 CC kit for performing gene detection by the invader assay. The method is
 CC useful for detecting a polymorphism in genes associated with
 CC osteoporosis, preferably postmenopausal osteoporosis. The method is also
 CC useful in an invader assay for detecting a gene. This polynucleotide
 CC sequence represents a primer used in the exemplification of the
 CC invention.


```
SQ Sequence 24 BP; 8 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 82.2%; Score 14.8; DB 14; Length 24;
Best Local Similarity 88.9%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18
DB 18 TGCCTTGAGAACTTAAGG 1

RESULT 3
ADW47302/c
ID ADW47302 standard; DNA; 29 BP.
XX
AC ADW47302;
XX
DT 07-APR-2005 (first entry)
XX
DE Osteoporosis polymorphism detection related primer, SEQ ID 8.
XX
KW SNP detection; osteoporosis; tumor necrosis factor receptor; TNFR;
KW DNA detection; ss; primer; PCR.
XX
OS Synthetic.
XX
XX JP2005006538-A.
XX
XX 13-JAN-2005.
XX
XX 18-JUN-2003; 2003JP-00173288.
XX
XX 18-JUN-2003; 2003JP-00173288.
XX
XX (UYNI-) UNIV NIPPON IKA.
XX
XX WPI; 2005-114728/13.
XX
XX Detecting polymorphism in genes associated with osteoporosis such as
XX tumor necrosis factor receptor associated factor binding protein gene,
XX reverse-inducible LIM domain protein gene and heat shock protein 70 gene.
XX
XX Disclosure; SEQ ID NO 8; 38pp; Japanese.
XX
XX The invention relates to a novel method for detecting polymorphism in
XX genes associated with osteoporosis, such as a tumor necrosis factor
XX receptor (TNFR) associated factor binding protein gene, reverse-inducible
XX LIM domain protein gene, heat shock protein 70 gene, or an alpha-2-
XX glycoprotein 1 gene. The invention further comprises: a kit for
XX performing gene detection, comprising components for detecting
XX polymorphism in genes associated with osteoporosis such as TNFR
XX associated factor binding protein gene, reverse-inducible LIM domain
XX protein gene, heat shock protein 70 gene, or an alpha-2-glycoprotein 1
XX gene; a kit for performing an invader assay, comprising components for
XX detecting polymorphisms chosen from polymorphism at base position 2141,
XX 1542 or 525 of TNFR associated factor binding protein gene, polymorphism
XX at base position 6364 in sequence of reverse-inducible LIM domain protein
XX gene, polymorphism at a base that encodes glutamic acid of position 110
XX in amino acid sequence of heat shock protein 70 gene, and polymorphism at
XX base position 1115 in base sequence of alpha-2-glycoprotein 1 gene; and a
XX kit for performing gene detection by the invader assay. The method is
XX useful for detecting a polymorphism in genes associated with
XX osteoporosis, preferably postmenopausal osteoporosis. The method is also
XX useful in an invader assay for detecting a gene. This polynucleotide
XX sequence represents a primer used in the exemplification of the
XX invention.
XX
XX Sequence 29 BP; 8 A; 3 C; 8 G; 10 T; 0 U; 0 Other;
Query Match 77.8%; Score 14; DB 14; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 20 BP; 3 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 76.7%; Score 13.8; DB 6; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTCGGG 18
DB 18 GCCTTGAGAACTTCAGG 2

RESULT 5
ACI93355/c
ID ACI93355 standard; DNA; 25 BP.
XX
XX ACI93355;
XX
```

DT 14-OCT-2003 (first entry)
 XX Human microarray DNA oligonucleotide SEQ ID NO 93346.
 DE EST; ss; probe; expressed sequence tag; microarray; gene expression;
 XX genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX Homo sapiens.
 OS
 XX
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PI Mittmann MP;
 XX
 DR WPI; 2003-567953/53.
 XX
 XX New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 93346; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 7 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
 Query Match 76.7%; Score 13.8; DB 9; Length 25;
 Best Local Similarity 88.2%; Pred. No. 2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TGCCCTTGAGAACTTCGG 17
 ||||| ||||| ||||| ||||| |||||
 Db 23 TGCCTTAAGAACGTCGG 7
 RESULT 6
 AAT10512
 ID AAT10512 standard; DNA; 30 BP.
 XX
 AC AAT10512;
 XX
 XX 12-JUL-1996 (first entry)
 DT
 XX

DE 5' primer for rabbit beta-globin intron amplification.
 XX
 KW transgenic mouse; thyroid hormone receptor; retinoic acid receptor;
 KW screen; antagonist; agonist; signal transduction mechanism; variant;
 KW primer; antisense; PCR; polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 PN JP07327548-A.
 XX
 PD 19-DEC-1995.
 XX
 PF 13-JUN-1994; 94JP-00154201.
 XX
 PR 13-JUN-1994; 94JP-00154201.
 XX
 PA (ONOY) ONO PHARM CO LTD.
 XX
 XX WPI; 1996-072216/08.
 DR
 XX Transgenic mouse contg. mutant human retinoic acid receptor alpha gene -
 PT used to screen for agonists or antagonists of human retinoic acid
 PT receptor, and elucidate the receptor's signal transduction mechanism.
 XX
 PS Example 2; Page 4; 7pp; Japanese.
 XX
 CC AAT10512-13 are used to PCR amplify a 0.7 kb rabbit beta-globin intron
 CC sequence, used in the construction of expression vector pG32-K14. The
 CC expression vector contains the keratin-14 promoter used to control a
 CC heterogenous gene, e.g. human retinoic acid receptor variant gene. The
 CC invention concerns generating transgenic mice contg. a gene (introduced
 CC under the control of the keratin-14 promoter) encoding a mutant human
 CC retinoic acid receptor alpha. These mice can be used to screen for
 CC (ant)agonists or to elucidate the signal transduction mechanism
 XX
 SQ Sequence 30 BP; 7 A; 4 C; 9 G; 10 T; 0 U; 0 Other;
 Query Match 74.4%; Score 13.4; DB 2; Length 30;
 Best Local Similarity 93.3%; Pred. No. 3.3e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 CTTGAGAACTTCGG 18
 ||||| ||||| ||||| ||||| |||||
 Db 8 CTTGAGAACTTCAGG 22
 RESULT 7
 ADO79688
 ID ADO79688 standard; DNA; 30 BP.
 XX
 AC ADO79688;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE DP33 PCR primer #22.
 XX
 KW Cytostatic; Gene therapy; breast cancer; human; DLG1; KIAA0783; DP33;
 KW CENPC1; SNP; single nucleotide polymorphism;
 KW D4, zinc and double PHD fingers, family 3; CERD4; cer-d4; FLJ14079;
 KW 2810403B03Rik; Rho family guanine-nucleotide exchange factor;
 KW chromosome 14q24.3-q31.1; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2004047514-A2.
 XX
 PD 10-JUN-2004.
 XX
 PF 25-NOV-2003; 2003WO-US037943.
 XX
 PR 25-NOV-2002; 2002US-0429136P.
 XX
 PR 24-JUL-2003; 2003US-0490234P.
 XX

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PA (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
XX
XX WPI; 2004-441037/41.
XX
XX Identifying a subject at risk of breast cancer by detecting the presence
XX of polymorphic variations in the DLG1, KIAA0783, DPf3 or CENPC1 regions
XX which are associated with breast cancer in a nucleic acid sample from a
XX subject.
XX
XX Example 5; Page 82; 227pp; English.
XX
XX The present invention relates to a method for identifying a subject at
XX risk of breast cancer. The method comprising detecting the presence or
XX absence of one or more polymorphic variations associated with breast
XX cancer in a nucleic acid sample from a subject. The nucleic acid sample
XX comprises the DLG1 region (AD079402), KIAA0783 region (AD079403), DPf3
XX region (AD079404) or CENPC1 region (AD079405). The gene DLG1 (discs,
XX large homolog 1 (Drosophila)) is also known as synapse-associated protein
XX 97, hdlg or SAP97. DLG1 has been mapped to chromosomal position 3q29. The
XX gene KIAA0783 is also known as PHF14 and PHD finger protein 14. KIAA0783
XX has been mapped to chromosomal position 7p21.3. The KIAA0783 protein is a
XX novel gene with unknown function, however, being a zinc finger protein,
XX it likely to be a transcription factor. The gene DPf3 (D4, zinc and
XX double PHD fingers, family 3) is also known as CERD4, cer-d4, FLJ14079
XX and 2810403803rik. DPf3 is a Rho family guanine-nucleotide exchange
XX factor. DPf3 has been mapped to chromosomal position 14q24.3-q31.1. The
XX gene CENPC1 (centromere protein C1) is also known as Centromere
XX autoantigen C1. CENPC1 has been mapped to chromosomal position 4q12-
XX q13.3. CENPC1 is a centromere autoantigen and a component of the inner
XX kinetochore plate. The CENPC1 protein is required for maintaining proper
XX kinetochore size and a timely transition to anaphase. The method is
XX useful for identifying a subject at risk of breast cancer, for early
XX diagnosis, prevention and treatment of breast cancer, to analyze and
XX predict a response to a breast cancer treatment, and in clinical drug
XX trials. The present sequence was used in an example from the invention.
XX
XX Sequence 30 BP; 6 A; 8 C; 7 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 74.4%; Score 13.4; DB 12; Length 30;
XX Best Local Similarity 93.3%; Pred. No. 3.3e+03;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 TGCCTTGAGAACTTC 15
XX ||||| |||||
XX Db 9 TGCCTTGAGAACTTC 23
XX
XX RESULT 8
XX ADY02087
XX ID ADY02087 standard; DNA; 30 BP.
XX
XX AC ADY02087;
XX
XX XX 05-MAY-2005 (first entry)
XX
XX DE PCR primer 791 used to amplify human DPf3 SNP DNA.
XX
XX XX SNP detection; breast tumor; endocrine disease;
XX KW gynecology and obstetrics; neoplasm; cytostatic; metastasis;
XX KW gene therapy; RNA interference; ss; PCR; primer;
XX KW D4, zinc and double PHD fingers, family 3; DPf3;
XX KW guanine-nucleotide exchange factor.
XX
XX OS Homo sapiens.
XX
XX XX WO2005014846-A2.
XX
XX PD 17-FEB-2005.
XX
XX XX 27-MAY-2004; 2004WO-US016939.
XX
XX

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PR 24-JUL-2003; 2003US-0490234P.
PR 25-NOV-2003; 2003US-00723681.
PR 25-NOV-2003; 2003US-0525239P.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
XX Hoyal-Wrightson CR;
XX
XX WPI; 2005-163257/17.
XX
XX Identifying risk of, preventing and/or treating breast cancer by
XX identifying and/or analyzing polymorphic variations in nucleotide
XX sequences within the human genome.
XX
XX Example 16; Page 245; 617pp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
XX of breast cancer comprising detecting the presence or absence of a
XX polymorphic variation associated with breast cancer. The method of the
XX invention demonstrates cytostatic activity and may be useful for
XX identifying a risk of, preventing and/or treating breast cancer and
XX cancer metastasis. The methods may be utilized for gene therapy or RNA
XX interference. The current sequence is that of a PCR primer of the
XX invention which was used to amplify a human rho-family guanine-nucleotide
XX exchange factor D4, zinc and double PHD fingers, family 3 (DPF3) DNA
XX containing a single nucleotide polymorphism (SNP).
XX
XX Sequence 30 BP; 6 A; 8 C; 7 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 74.4%; Score 13.4; DB 14; Length 30;
XX Best Local Similarity 93.3%; Pred. No. 3.3e+03;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 TGCCTTGAGAACTTC 15
XX ||||| |||||
XX Db 9 TGCCTTGAGAACTTC 23
XX
XX RESULT 9
XX ADT75569/c
XX ID ADT75569 standard; DNA; 20 BP.
XX
XX AC ADT75569;
XX
XX DT 13-JAN-2005 (first entry)
XX
XX XX S. pneumoniae PCR primer SEQ ID NO 277.
XX
XX DE Streptococcus pneumoniae; cpsA; cpsB; wzy; wzx; microarray; serotype; ss;
XX KW PCR; primer.
XX
XX OS Streptococcus pneumoniae.
XX
XX XX WO2004090159-A1.
XX
XX PD 21-OCT-2004.
XX
XX PF 13-APR-2004; 2004WO-AU0000480.
XX
XX PR 10-APR-2003; 2003AU-00901717.
XX
XX PA (WSD-) WESTERN SYDNEY AREA HEALTH SERVICE.
XX PA (TIAN-) TIANJIN BIOCHIP TECHNOLOGY CORP.
XX
XX Kong F, Gilbert G, Wang L, Liu D, Tao J;
XX WPI; 2004-748779/73.
XX
XX Determining Streptococcus pneumoniae serotypes, useful in monitoring the
XX epidemiology of invasive S. pneumoniae infections, comprises analyzing
XX cpsA and cpsB gene and/or wzy and/or wzx gene.
XX

```

PS Claim 14; SEQ ID NO 277; 323pp; English.

CC The invention relates to a method of distinguishing/determining between
CC at least 25 different serotypes of Streptococcus pneumoniae in a sample
CC which comprises analysing at least a portion of the nucleotide sequence
CC between the 3' end of the cpsA gene and the 5' end of the cpsB gene
CC and/or at least a portion of the wzy and/or wzx gene(s). The microarray
CC is useful for serotyping a strain of S. pneumoniae. The method and
CC polynucleotides are useful for distinguishing/determining different
CC serotypes of S. pneumoniae in a sample. The methods, probes/primer and
CC microarrays are useful in monitoring the epidemiology of invasive S.
CC pneumoniae infections to assist in disease control and in informing
CC vaccine policy. The present sequence represents a S. pneumoniae PCR
CC primer.

SQ Sequence 20 BP; 8 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 13; Length 20;

Best Local Similarity 83.3%; Pred. No. 4.1e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTTCGGG 18

Db 19 TGCTTTGAGAACTTCGG 2

RESULT 10

AAQ70160/c

ID AAQ70160 standard; DNA; 29 BP.

XX AAQ70160;

DT 10-APR-1995 (first entry)

DE Primer for Japanese encephalitis virus antigen coding sequence.

XX Chimeric; chimera; vaccine; multivalent; hepatitis B virus; HBV;

KW hepatitis; Japanese encephalitis virus; baculovirus; ss.

XX Synthetic.

OS JP06205672-A.

PN 26-JUL-1994.

PD 19-MAR-1992; 92JP-00063699.

XX 19-MAR-1992; 92JP-00063699.

XX (JAPG) NIPPON ZEON KK.

PA (TOKS-) TOKYO SHINKEI KAGAKU SOGO KENKYUSHO ZH.

XX WPI; 1994-275516/34.

XX Prodn. of chimeric proteins having antigenic sites from Japanese

PT encephalitis virus and hepatitis B virus surface antigens - also

PT recombinant baculovirus, useful as multivalent vaccine.

XX Example 1; Page 4; 13pp; Japanese.

XX Two primers (AAQ70159, AAQ70160) were used to amplify a sequence encoding
CC an antigen from Japanese encephalitis virus for its use in the
CC construction of a chimeric protein designated R3:S. The chimeric protein
CC comprises antigenic sites from Japanese encephalitis virus and Hepatitis
CC B virus surface antigens. The protein may be used as a multivalent
CC vaccine. This primer was also used alongside a second primer to amplify
CC another antigen coding sequence used in the construction of a similar
CC chimeric protein. See also AAQ70159-65

SQ Sequence 29 BP; 9 A; 10 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 2; Length 29;

Best Local Similarity 83.3%; Pred. No. 4.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTTCGGG 18

Db 18 TGCTTTGAGAACTTCGAG 1

RESULT 11

AAA77010

ID AAA77010 standard; cDNA; 51 BP.

XX AAA77010;

DT 16-NOV-2000 (first entry)

DE Human clone c943054295 polymorphic site, SEQ ID NO:693.

XX Human; single nucleotide polymorphism; SNP; chromosome X; detection;
KW identification; gene therapy; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FT variation replace(26,G)
FT /*tag= a

PN WO200029623-A2.

XX 25-MAY-2000.

XX 17-NOV-1999; 99WO-US027293.

XX 17-NOV-1998; 98US-0109024P.

PR 16-NOV-1999; 99US-00443199.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach MD;

XX WPI; 2000-387826/33.

XX Human nucleic acids containing single nucleotide polymorphisms, useful
PT for treating a subject suffering, or at risk from a pathology due to the
PT presence of a sequence polymorphism.

PS Claim 1; Page 367; 543pp; English.

XX Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112
CC (AAA76318-A77429) are consecutive pairs of nucleotides which contain
CC silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are consecutive
CC pairs of nucleotides containing SNPs which result in changes in the
CC corresponding amino acid sequences (AAB11749-B11828). The SNPs in
CC sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
CC changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
CC in non-conservative changes. The SNPs in sequences 1187 to 1192
CC (AAA77504-A77509) generate frameshift mutations. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic
CC proteins/peptides using the antibodies. The nucleic acids are useful for
CC gene therapy of an individual having, suspected of having, or at risk of
CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the wild-
CC type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals

XX Sequence 51 BP; 8 A; 12 C; 22 G; 9 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 3; Length 51;

Best Local Similarity 83.3%; Pred. No. 4.6e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy
Db

1 TGCCTTGAGAACTTCGGG 18
|||
33 TGCTTAGAGACCTTCGGG 50

RESULT 12

AAA77011
ID AAA77011 standard; cDNA; 51 BP.

AC AAA77011;

16-NOV-2000 (first entry)

DE Human clone cq43054295 polymorphic site, SEO ID NO:694.

Human; single nucleotide polymorphism; SNP; chromosome X; detection; identification; gene therapy; ss.

OS Homo sapiens.

XX		
FH	Key	Location/Qualifiers
FT	variation	replace(26,C)
FT		/tag= a

WO200029623-A2.

25-MAY-2000.

17-NOV-1999; 99WO-US027293.

PR 17-NOV-1998; 98US-0109024P.

PR 16-NOV-1999; 99US-00443199;

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach MD;

DR WPI; 2000-387826/33.

Human nucleic acids containing single nucleotide polymorphisms, useful for treating a subject suffering, or at risk from a pathology due to the presence of a sequence polymorphism.

PS Claim 1: Page 367: 543pp: English.

Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences which contain single nucleotide polymorphisms (SNPs). Sequences 1 to 1112 (AAA76318-A77429) are consecutive pairs of nucleotides which contain silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are consecutive pairs of nucleotides containing SNPs which result in changes in the corresponding amino acid sequences (AAB11749-B11828). The SNPs in sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result in non-conservative changes. The SNPs in sequences 1187 to 1192 (AAA77504-A77509) generate frameshift mutations. The invention also relates to a method of detecting a polymorphic site in a nucleic acid and a method of determining the relatedness of two nucleic acids. It also encompasses peptides containing polymorphic sites, antibodies raised against such peptides, and a method of detecting polymorphic proteins/peptides using the antibodies. The nucleic acids are useful for gene therapy of an individual having, suspected of having, or at risk of developing a pathological condition due to the presence of a sequence polymorphism. Such treatment would comprise administration of the wild-type nucleic acid sequence. Antibodies raised against polymorphic peptides can also be used in the treatment of such individuals

Sequence 51 BP; 8 A; 11 C; 23 G; 9 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 3; Length 51;
Best Local Similarity 83.3%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels

Qy 1 TGCCTTGAGAACTTCGGG 18
Db 33 TGCTTAGAGACCTTCGGG 50

RESULT 13

AAL27669
 ID AAL27669 standard; DNA; 51 BP.

AC AAL27669:

24-JAN-2002 (first entry)

Human SNP oligonucleotide #877.

KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
 KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease. ss.

OS Homo sapiens.

PN WO200147944-A2.

05-JUL-2001.
PD
XX

28-DEC-2000; 2000WO-US035498.

PR 28-DEC-1999: 99US-0173419P.

27-DEC-2000; 2000US-00173419.
PR

PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA. Leach M:

WPI: 2001-465210/50.

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.

PS Claim 1: Page 1633: 4143pp: English.

The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiotensin, apolipoprotein related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.

Sequence 51 BP; 12 A; 19 C; 14 G; 6 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 4; Length 51;
Best Local Similarity 83.3%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels

Qy 1 TGCCTTGAGAACTTCGG 18
|||
db 25 TGCCTCCAGAACTCCGG 42

RESULT 14

ADQ07709

ID ADQ07709 standard; DNA; 60 BP.

XX AC

XX ADQ07709;

XX AC

DT 09-SEP-2004 (first entry)

XX AC

DE PCR primer for a talin open reading frame.

XX AC

KW trap vector; Gateway technology; homologous recombination; PCR; primer;

KW ss; talin.

XX AC

OS Synthetic.

XX AC

PN WO2004053123-A1.

XX AC

PD 24-JUN-2004.

XX AC

PF 04-DEC-2003; 2003WO-JP015571.

XX AC

PR 10-DEC-2002; 2002JP-00357566.

XX AC

PA (KAZU-) KAZUSA DNA RES INST FOUND.

XX AC

PI Negase T, Nakajima D, Ohara O;

XX AC

DR WPI; 2004-480936/45.

XX AC

XX New template vector for trap vectors comprises a replication origin, a

PT drug tolerance gene, first and second primer binding sequences, and a

PT suicide gene interposed between the primer binding sequences.

XX AC

PS Example 2; Page 16; 34pp; Japanese.

XX AC

The specification describes a template vector for trap vectors containing a replication origin, a drug tolerance gene, a primer binding sequence, a second primer binding sequence and a suicide gene interposed between the first and second primer binding sequences. The cloning vector is useful as an entry clone in Gateway (RTM) technology. The target open reading frame (ORF) can be accurately, quickly and conveniently cloned by homologous recombination. The present sequence represents a PCR primer which is used to amplify a talin ORF. The amplified fragment is used in the course of the invention.

XX AC

SQ Sequence 60 BP; 15 A; 16 C; 13 G; 15 T; 0 U; 1 Other;

Query Match 73.3%; Score 13.2; DB 12; Length 60;

Best Local Similarity 83.3%; Pred. No. 4.7e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18

||||| ||| ||||| |

Db 17 TGCCTTCAGAGCTTCGAG 34

RESULT 15

ABN52445

ID ABN52445 standard; DNA; 65 BP.

XX AC

XX ABN52445;

XX AC

XX 15-JUL-2002 (first entry)

XX AC

DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:25193.

XX AC

KW Human; mouse; rat; splice transcript; detection; RNA transcript;

XX AC

KW splice variant; transcriptome; oligonucleotide library; ss.

XX AC

OS Mus musculus.

XX AC

PN WO200210449-A2.

XX AC

PD 07-FEB-2002.

XX AC

XX 20-JUL-2001; 2001WO-IB001903.

XX AC

XX 28-JUL-2000; 2000US-0221607P.

XX AC

XX 02-MAY-2001; 2001US-0287724P.

XX AC

PA (COMP-) COMPUGEN INC.

XX AC

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX AC

XX WPI; 2002-257383/30.

XX AC

New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes.

XX AC

PS Example 1; SEQ ID NO 25193; 47pp; English.

XX AC

The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue - and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX AC

SQ Sequence 65 BP; 10 A; 19 C; 18 G; 18 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 6; Length 65;

Best Local Similarity 83.3%; Pred. No. 4.7e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18

||||| ||| ||||| |

Db 3 TGCCTTCAGTACTTCGTG 20

RESULT 16

AAQ79424/c

ID AAQ79424 standard; DNA; 21 BP.

XX AC

XX AAQ79424;

XX AC

XX 25-MAR-2003 (revised)

XX AC

XX 03-JUN-1995 (first entry)

XX AC

DE PCR primer no. 12 based on human hepatocyte inducible nitric oxide

XX AC

DE synthase (iNOS) cDNA.

XX AC

KW Nitric oxide synthase; diabetes mellitus; PCR primer; ss.

XX AC

XX Synthetic.

XX AC

PN WO9424269-A1.
XX
PD 27-OCT-1994.
XX
XX 11-APR-1994; 94WO-DK000146.
PF
XX 16-APR-1993; 93DK-00000433.
PR
XX (NOVO) NOVO-NORDISK AS.
PA
XX Karlsen AE;
PI
XX WPI; 1994-341851/42.
DR
XX
XX New DNA encoding inducible pancreatic islet nitric oxide synthase - and
PT related vectors and transformed cells, useful for identifying specific
PT inhibitors for treatment or prevention of insulin dependent diabetes
PT mellitus.
XX
PS Example; Page 25; 36pp; English.
XX
XX Human islets were incubated in a mixture of IL-1, TNF-alpha and IFN-
CC gamma. The human islet iNOS was cloned by RT-PCR on the isolated mRNA
CC with primers based on the human hepatocyte sequence. The sequence of the
CC primers is given in AAQ79424 and AAQ79425. The clone human islet iNOS was
CC sequenced. The 5' UTR and translated human islet iNOS is given in
CC AAQ79426, and the 3' end in AAQ79427. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
XX Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
SQ
Query Match 72.2%; Score 13; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGCCTTGAGAACT 13
DB 13 TGCCTTGAGAACT 1
RESULT 17
ADD41511/c
ID ADD41511 standard; DNA; 50 BP.
XX
XX AC
XX ADD41511;
XX
DT 15-JAN-2004 (first entry)
XX
DE Synthetic insecticidal toxin gene (cryIAC) production PCR primer #54.
XX
XX synthetic insecticidal toxin gene; cryIAC; diamondback moth; PCR; primer;
XX ss.
XX
OS Synthetic.
OS Unidentified.
XX
XX KR2002013003-A.
PN
XX 20-FEB-2002.
PD
XX
XX 10-AUG-2000; 2000KR-00046327.
PF
XX 10-AUG-2000; 2000KR-00046327.
PR
XX (RURA-) RURAL DEV ADMINISTRATION.
PA
XX Cho HS, Jin YM, Kim HI, Park BS;
PI
XX WPI; 2002-747866/81.
DR
XX Synthetic insecticidal toxin gene for transformation of brassica plants.
PT
XX Example 2; Page 15; 23pp; Korean.
PS

XX The invention comprises a synthetic insecticidal toxin gene (cryIAC) for
CC the transformation of Brassicae plants. The cryIAC gene is useful for
CC preventing plants from being damaged by the diamondback moth (Plutella
CC xylostella). The present DNA sequence represents a PCR primer that was
CC used in the construction of the cryIAC gene of the invention.
XX
SQ Sequence 50 BP; 16 A; 10 C; 14 G; 10 T; 0 U; 0 Other;
Query Match 72.2%; Score 13; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CTTGAGAACTTCG 16
DB 33 CTTGAGAACTTCG 21

RESULT 18
ADM68520
ID ADM68520 standard; DNA; 63 BP.
XX
XX AC ADM68520;
XX
DT 03-JUN-2004 (first entry)
XX
XX BtSlm related oligonucleotide #17.
XX
XX Insecticidal protein; BtSlm; ss.
XX
OS Synthetic.
XX CN1393561-A.
PN
XX 29-JAN-2003.
PD
XX 22-JUN-2001; 2001CN-00129519.
PF
XX 22-JUN-2001; 2001CN-00129519.
PR
XX (MICR-) INST MICROBES CHINESE ACAD SCI.
PA
XX Tian Y, Qin H, Guo H;
PI
XX WPI; 2003-469217/45.
XX
XX Mosaic insecticidal protein gene able to secrete its product to outside
PT of cell.
XX
XX Example 1; Page 14; 46pp; Chinese.
XX
XX The present invention relates to an artificially synthetic mosaic
CC insecticidal protein gene BtIm of Bacillus thuringiensis (Bt) which can
CC be effectively expressed in higher plant. By adding a secretory signal
CC peptide coding sequence to the terminal 5' of the said gene can generate
CC a fusion protein gene BtSlm (ADM68502). The insecticidal protein Bt
CC (ADM68503) expressed by the gene in plant can be secreted in the gap
CC between cells, so improving the stability of insecticidal protein and
CC reducing the interference of insecticidal protein to normal cell
CC function. The present sequence was used to illustrate the invention.
XX
SQ Sequence 63 BP; 14 A; 17 C; 16 G; 16 T; 0 U; 0 Other;
Query Match 72.2%; Score 13; DB 11; Length 63;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CTTGAGAACTTCG 16
DB 13 CTTGAGAACTTCG 25

RESULT 19

ABN51708
ID ABN51708 standard; DNA; 65 BP.
XX AC
AC ABN51708;
XX DT
DT 15-JUL-2002 (first entry)
XX DE
DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:24456.
XX KW
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX OS
OS Mus musculus.
XX PN
PN WO200210449-A2.
XX PD
PD 07-FEB-2002.
XX PF
PF 20-JUL-2001; 2001WO-IB001903.
XX PR
PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX PA
PA (COMP-) COMPUGEN INC.
XX PI
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX DR
DR WPI; 2002-257383/30.
XX PT
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX PS
PS Example 1; SEQ ID NO 24456; 47pp; English.
XX CC
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridizing selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ
SQ Sequence 65 BP; 13 A; 20 C; 17 G; 15 T; 0 U; 0 Other;

Query Match 72.2%; Score 13; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TGAGAACTTCGG 18
DB 10 TGAGAACTTCGG 22

RESULT 20
ADP18282

ADP18282 standard; DNA; 20 BP.
ADP18282;
29-JUL-2004 (first entry)
HEX1 gene antisense primer seqid 24.
cytostatic; senescence; cell proliferation; neoplastic cell growth;
cellular gene expression; reverse transcriptase PCR; RT-PCR; primer; ss;
doxorubicin-induced senescence; HCT 116 cell; human.
Homo sapiens.
US2004058320-A1.
25-MAR-2004.
21-DEC-2001; 2001US-00032264.
21-DEC-2000; 2000US-0257907P.
17-DEC-2001; 2001US-0341425P.
(RONI/) RONINSON I B.
(CHAN/) CHANG B.
Roninson IB, Chang B;
WPI; 2004-294237/27.
Identifying a compound that induces senescence in a mammalian cell,
useful for treating abnormal cell proliferation, comprises assaying
expression of a cellular gene in the cell in the presence and in the
absence of a compound.
Example 2; SEQ ID NO 24; 29pp; English.
The invention describes a method of identifying a compound that induces
senescence in a mammalian cell. The method comprises: culturing the
mammalian cell in the presence and absence of the compound; assaying the
expression of at least one cellular gene selected from 73 genes given in
the specification, in the cell in the presence and in the absence of the
compound; and identifying compounds that induce senescence when
expression of at least one of the cellular gene is higher in the presence
of the compound than in the absence of the compound. Also described are:
a compound that induces senescence in a mammalian cell identified from
the method above; assessing efficacy of a treatment of a disease or
condition relating to abnormal cell proliferation or neoplastic cell
growth; and identifying a compound that inhibits senescence-associated
induction of cellular gene expression. Compounds that induce senescence
in abnormally proliferating or neoplastic cells are useful for treating a
disease or condition relating to abnormal cell proliferation or
neoplastic cell growth. This sequence represents a reverse transcriptase
PCR primer used to identify genes induced and repressed following
doxorubicin-induced senescence of HCT 116 cells.
Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 12; Length 20;
Best Local Similarity 87.5%; Pred. No. 6.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTCGG 17
DB 2 GCCTTGAGAACTTCAG 17

RESULT 21
ABQ03710/c
ID ABQ03710 standard; DNA; 24 BP.
XX AC
XX ABQ03710;
XX

DT 11-JUN-2002 (first entry)
XX Oligonucleotide adapter/capture probe 3701.
XX Oligonucleotide array; adapter sequence; probe; ss.
OS Synthetic.
XX WO200216649-A2.
XX 28-FEB-2002.
XX 27-AUG-2001; 2001WO-US026519.
XX 25-AUG-2000; 2000US-0227948P.
XX 29-AUG-2000; 2000US-0228854P.
XX (ILLU-) ILLUMINA INC.
XX Gunderson K;
XX WPI; 2002-292068/33.
XX Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.
XX Claim 1; Page 132; 261pp; English.
XX The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ0010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ0010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
XX Sequence 24 BP; 6 A; 8 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 71.1%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 6.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TGCCTTGAGACTTCG 16
Db 23 TGCCTAGACATCTCG 8
RESULT 22
ADY26567/c
ID ADY26567 standard; DNA; 36 BP.
XX AC ADY26567;
XX 05-MAY-2005 (first entry)
XX PCR primer #1 used to amplify DNA encoding a human dicer mutant.
XX dsRNA degradation; dicer; RNaseIIa; RNaseIIb; PAZ domain; PCR; primer; ss.
XX Homo sapiens.
XX Synthetic.
XX WO2005017144-A1.
XX 24-FEB-2005.
XX 10-AUG-2004; 2004WO-JP011480.
XX 14-AUG-2003; 2003JP-00293553.

PR 30-SEP-2003; 2003JP-00342126.
PR 08-DEC-2003; 2003JP-00409639.
PR 24-MAR-2004; 2004JP-00086129.
XX (TAKI) TAKARA BIO INC.
XX Sagawa H, Tomono J, Ueno H, Kato I;
XX WPI; 2005-182369/19.
XX Methods for degrading dRNAs and synthesizing RNAs of definite length, comprises employing specific enzymatic proteins, used e.g. in RNA interference and other applications in medical and biological fields.
XX Example 1; SEQ ID NO 5; 56pp; Japanese.
XX The specification describes a protein with a dsRNA degrading activity, that is capable of acting on a dsRNA to form a dsRNA of a definite length. The protein has a functional domain of dicer which is composed of RNaseIIa and b as well as a dsRNA-binding domain, particularly a PAZ domain too. The protein of the invention is useful for degrading dRNAs and synthesizing RNAs of definite length which are useful, e.g. for RNA interference and in other applications in medical and biological fields particularly and genetic engineering. PCR primers ADY26567-ADY26568 were used to amplify DNA encoding a human dicer protein mutant.
XX Sequence 36 BP; 8 A; 10 C; 12 G; 6 T; 0 U; 0 Other;
Query Match 71.1%; Score 12.8; DB 14; Length 36;
Best Local Similarity 87.5%; Pred. No. 7.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 CCTTGAGACTTCGGG 18
Db 28 CCTTGAGACTTCGGG 13
RESULT 23
ABK88169/c
ID ABK88169 standard; DNA; 41 BP.
XX AC ABK88169;
XX 07-OCT-2002 (first entry)
XX Human nucleotide excision repair protein 13.75, probe #1.
XX Human; nucleotide excision repair protein 13.75;
XX embryo development distortion; tumour; Cockayne syndrome; probe; ss.
XX Homo sapiens.
XX CN1340517-A.
XX 20-MAR-2002.
XX 31-AUG-2000; 2000CN-00119815.
XX 31-AUG-2000; 2000CN-00119815.
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX Mao Y, Xie Y;
XX WPI; 2002-436411/47.
XX Polypeptide-human nucleotide excision repair protein 13.75 and polynucleotide for coding it.
XX Example 6; Page 21 (Disclosure); 35pp; Chinese.
XX The invention describes a novel polypeptide-human nucleotide excision repair protein 13.75, the polynucleotide encoding it and the process for

CC preparing the polypeptide by DNA recombination. The protein is useful for
CC treating diseases such as embryo development distortion, tumour and
CC Cockayne syndrome. The antagonist against this polypeptide and its
CC therapeutic action, and the application of the polynucleotide to coding
CC this new human nucleotide excision repair protein 13.75 are also
CC disclosed. This sequence represents a probe used to detect cDNA encoding
CC the human nucleotide excision repair protein 13.75

XX
SQ Sequence 41 BP; 10 A; 8 C; 14 G; 9 T; 0 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 6; Length 41;
Best Local Similarity 87.5%; Pred. No. 7.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTCGG 17
|||||
Db 34 GCCTTGAGAACTTCGG 19

RESULT 24
ABX15037
ID ABX15037 standard; DNA; 22 BP.
XX AC
XX ABX15037;
XX
DT 17-MAR-2003 (first entry)
XX
DE Human beta-defensin-1 real-time PCR primer #1.
XX
KW Human; ss; PCR; primer; real-time PCR; otitis media; antimicrobial;
KW paranasal sinusitis; lysozyme; beat-defensin 1; beta-defensin 2;
KW lactoferrin; auditory; antiinflammatory.
XX
OS Homo sapiens.
XX
PN US2002141986-A1.
XX
PD 03-OCT-2002.
XX
PF 27-NOV-2001; 2001US-00998547.
XX
PR 28-NOV-2000; 2000US-0253492P.
XX
PA (LIMD/) LIM D J.
PA (LEEH/) LEE H.
PA (WEBS/) WEBSTER P.
PA (ANDA/) ANDALIBI A.
PA (LIJG/) LI J.
PA (GANZ/) GANZ T.
XX
PI Lim DJ, Lee H, Webster P, Andalibi A, Li J, Ganz T;
XX WPI; 2003-174127/17.
XX
PT New pharmaceutical preparation comprising lactoferrins, lysozyme or
PT defensins in an amount effective to reduce the growth of microbes, a salt
PT chelator, and a carrier, useful for treating of otitis media and
PT paranasal sinusitis.
XX
PS Example 1; Page 7; 23pp; English.
XX
CC The invention relates to a pharmaceutical preparation for the treatment
CC of otitis media and sinusitis, comprising at least one component, such as
CC lactoferrins, lysozyme or defensins (e.g. beta-defensin 1 or 2) in an
CC amount effective to reduce the growth of microbes, a salt chelator, and a
CC carrier. Also included is a method for treating microbial infections in a
CC mammal by administering to the mammal the pharmaceutical composition
CC cited above to reduce the number of causative infective agents. The
CC pharmaceutical preparation is useful for treating microbial infections of
CC the ear and sinuses, e.g. otitis media or paranasal sinusitis. The
CC invention provides molecules that are unlikely to induce antibiotic
CC resistance as compared to the existing antibiotics. These molecules do
CC not induce allergic reactions, since they are produced by the host. The

CC method of the invention is more cost-effective than the antibiotic
CC treatment. The present sequence is a real-time PCR primer used to assay
CC the expression of human beta-defensin-1 in infected and normal middle ear

XX
SQ Sequence 22 BP; 5 A; 8 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 68.9%; Score 12.4; DB 8; Length 22;
Best Local Similarity 92.9%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTC 15
|||||
Db 2 GCCATGAGAACTTC 15

RESULT 25
ADW12549
ID ADW12549 standard; DNA; 22 BP.
XX AC
XX ADW12549;
XX
DT 24-MAR-2005 (first entry)
XX
DE Human beta-defensin-1 amplifying forward RT-PCR primer.
XX
KW Pharmaceutical; chemotherapy; therapy; otitis media; sinusitis;
KW ear, nose, throat disease; infection; inflammation; respiratory disease;
KW antimicrobial; auditory; antiinflammatory; antibacterial; RT-PCR;
KW reverse transcriptase PCR; primer; beta-defensin; ss.
XX
OS Homo sapiens.
XX
PN US2004265296-A1.
XX
PD 30-DEC-2004.
XX
PF 06-APR-2004; 2004US-00819714.
XX
PR 28-NOV-2000; 2000US-0253492P.
PR 27-NOV-2001; 2001US-00998547.
XX
PA (LIMD/) LIM D J.
PA (LEEH/) LEE H.
PA (WEBS/) WEBSTER P.
PA (ANDA/) ANDALIBI A.
PA (LIJG/) LI J.
PA (GANZ/) GANZ T.
XX
PI Lim DJ, Lee H, Webster P, Andalibi A, Li J, Ganz T;
XX WPI; 2005-064869/07.
XX
PT Pharmaceutical preparation, useful for the treatment of microbial
PT infections of the ear and sinuses, comprises at least one of
PT lactoferrins, lysozyme or defensins, a salt chelator and a carrier.
XX
PS Example 1; SEQ ID NO 5; 25pp; English.
XX
CC The present invention relates to a pharmaceutical preparation comprising
CC at least one of lactoferrins (LF), lysozyme (Lz), beta-defensins (BD), a
CC salt chelator and a carrier. The invention is useful in the treatment of
CC otitis media (OM) and sinusitis. The present sequence is the human beta-
CC defensin-1 amplifying RT (reverse transcriptase)-PCR primer.
XX
SQ Sequence 22 BP; 5 A; 8 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 68.9%; Score 12.4; DB 14; Length 22;
Best Local Similarity 92.9%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTC 15
|||||
Db 2 GCCATGAGAACTTC 15

Search completed: March 3, 2006, 08:00:33
Job time : 123.534 secs

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98 11.6 64.4 55 3 US-08-956-171E-2263 Sequence 2263, Ap
99 11.6 64.4 55 3 US-08-781-986A-2263 Sequence 2263, Ap
c 100 11.4 63.3 15 2 US-08-456-840-33 Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-09-657-042A-36/c
; Sequence 36, Application US/09657042A
; Patent No. 6329203
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-1 EXPRESSION
; FILE REFERENCE: RTS-0148
; CURRENT APPLICATION NUMBER: US/09/657,042A
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-657-042A-36

Query Match 76.7%; Score 13.8; DB 3; Length 20;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTCGGG 18
|||||
Db 18 GCCTTGAGAACTTCAGG 2

RESULT 2
US-10-131-827-8979
; Sequence 8979, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fty, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8979
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-131-827-8979

Query Match 73.3%; Score 13.2; DB 3; Length 21;
Best Local Similarity 83.3%; Pred. No. 9.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18
|||||
Db 3 TGCCTTGAGAACTTCGAG 20

RESULT 3
US-09-396-196G-1069/c
; Sequence 1069, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1069
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-1069

Query Match 73.3%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 9.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18
|||||
Db 19 TGCCTTGAGAACTTCGAG 2

RESULT 4
US-09-396-196G-54888/c
; Sequence 54888, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: David Lockhart
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54888
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-54888

Query Match 73.3%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 9.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGGG 18
|||||
Db 20 TGCCTTGAGAACTTCGAG 3

RESULT 5
US-09-396-196G-68119
; Sequence 68119, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54889
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-54889

Query Match 68.9%; Score 12.4; DB 3; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTT 14
|||||
Db 14 TGCCTTGAGAACTT 1

RESULT 10
US-09-396-196G-75625/c
; Sequence 75625, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75625
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-75625

Query Match 68.9%; Score 12.4; DB 3; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CTTGAGAACTTCGG 17
|||||
Db 23 CTTGAGAACTTAGG 10

RESULT 11
US-09-396-196G-75626/c
; Sequence 75626, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 75626
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-75626

Query Match 68.9%; Score 12.4; DB 3; Length 25;
Best Local Similarity 92.9%; Pred. No. 2.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CTTGAGAACTTCGG 17
|||||
Db 17 CTTGAGAACTTAGG 4

RESULT 12
US-08-991-525B-86/c
; Sequence 86, Application US/08991525B
; Patent No. 6093811
; GENERAL INFORMATION:
; APPLICANT: Bennett and Mirabelli
; TITLE OF INVENTION: Oligonucleotide Modulation
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WORDPERFECT 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,525B
; FILING DATE: December 16, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 440,740
; FILING DATE: May 12, 1995
; PRIOR APPLICATION DATA: 063,167
; APPLICATION NUMBER: 063,167
; FILING DATE: May 17, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 969,151
; FILING DATE: February 10, 1993
; PRIOR APPLICATION DATA: 007,997
; APPLICATION NUMBER: 939,855
; FILING DATE: September 2, 1992
; PRIOR APPLICATION DATA: 567,286
; APPLICATION NUMBER: 567,286
; FILING DATE: August 14, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-991-525B-86

Query Match 68.9%; Score 12.4; DB 3; Length 32;
Best Local Similarity 92.9%; Pred. No. 2.7e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTTGAGAACTTCG 17
|||||
Db 31 CTTGAGAACTTCAG 18

RESULT 13
US-08-456-840-11/c
; Sequence 11, Application US/08456840
; Patent No. 5597908
; GENERAL INFORMATION:
; APPLICANT: Taddei-Peters, W. C.
; APPLICANT: Butler, Sandra M.
; TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5597908el
; STREET: 1330 Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: US
; ZIP: 20850

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,840
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/266,407
; FILING DATE: 27-JUN-1994
; APPLICATION NUMBER: US 08/172,461
; FILING DATE: 21-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELEPHONE: 301-258-5200
; TELEFAX: 301-977-0847
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..39
US-08-456-840-11

Query Match 68.9%; Score 12.4; DB 2; Length 39;
Best Local Similarity 92.9%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTC 15
|||||
Db 25 GCCTTGAGAACTTC 12

RESULT 14
US-08-266-407A-11/c
; Sequence 11, Application US/08266407A
; Patent No. 5786156
; GENERAL INFORMATION:

; APPLICANT: Taddei-Peters, W. C.
; APPLICANT: Butler, Sandra M.
; TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5786156el
; STREET: 1330 Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: US
; ZIP: 20850

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/266,407A
; FILING DATE: 27-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/172,461
; FILING DATE: 21-DEC-1993
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-258-5200
; TELEFAX: 301-977-0847
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..39
US-08-266-407A-11

Query Match 68.9%; Score 12.4; DB 2; Length 39;
Best Local Similarity 92.9%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTC 15
|||||
Db 25 GCCTTGAGAACTTC 12

RESULT 15
US-08-892-544-11/c
; Sequence 11, Application US/08892544
; Patent No. 5874544
; GENERAL INFORMATION:
; APPLICANT: Taddei-Peters, W. C.
; APPLICANT: Butler, Sandra M.
; TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5874544el
; STREET: 1330 Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: US
; ZIP: 20850

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/892,544
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US/08/266,407
; APPLICATION NUMBER: 27-JUN-1994
; FILING DATE: 27-JUN-1994
; APPLICATION NUMBER: US 08/172,461
; FILING DATE: 21-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-258-5200
; TELEFAX: 301-977-0847
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..39
; US-08-892-544-11

Query Match      68.9%; Score 12.4; DB 2; Length 39;
Best Local Similarity 92.9%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCCTTGAGAACTTC 15
        |||||
Db      25 GCCTTGAGAACTTC 12

RESULT 16
US-07-982-712-14
; Sequence 14, Application US/07982712
; Patent No. 5436391
; GENERAL INFORMATION:
; APPLICANT: Hideyo FUJIMOTO, Kimiko ITOH
; APPLICANT: Mikihiro YAMAMOTO, and Ko SHIMAMOTO
; TITLE OF INVENTION: Insecticidal Protein-encoding Gene, Gramineous
; TITLE OF INVENTION: Plants Transformed with the Gene, and Production Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/982,712
; FILING DATE: 19921127
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
```

```
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-07-982-712-14

Query Match      68.9%; Score 12.4; DB 2; Length 68;
Best Local Similarity 92.9%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 CCTTGAGAACTTCG 16
        |||||
Db      21 CCTTGAGAACTTCG 34

RESULT 17
US-09-149-727-59/c
; Sequence 59, Application US/09149727
; Patent No. 6391547
; GENERAL INFORMATION:
; APPLICANT: Jefferson, Richard A.
; APPLICANT: Kilian, Andrzej
; APPLICANT: Keese, Paul Konrad
; TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 190106.405
; CURRENT APPLICATION NUMBER: US/09/149,727
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: US 60/058,263
; EARLIER FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide. Product of Synthesis to Overlap
; OTHER INFORMATION: and create fragments of engineered secretatable
; OTHER INFORMATION: microbial GUS (Figure 13)
; US-09-149-727-59

Query Match      68.9%; Score 12.4; DB 3; Length 80;
Best Local Similarity 92.9%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 TTGAGAACTTCGG 18
        |||||
Db      48 TTGAGAACTTCGTG 35

RESULT 18
US-09-270-957-98/c
; Sequence 98, Application US/09270957
; Patent No. 6641996
; GENERAL INFORMATION:
; APPLICANT: Richard A. Jefferson and Jorge E. Mayer
; TITLE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, GENE
; TITLE OF INVENTION: PRODUCTS, AND USES THEREOF
; FILE REFERENCE: 190106.405C1
; CURRENT APPLICATION NUMBER: US/09/270,957
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Oligonucleotide. Product of synthesis to overlap
; OTHER INFORMATION: and create fragments of an engineered secretatable
; OTHER INFORMATION: microbial GUS
US-09-270-957-98

Query Match 68.9%; Score 12.4; DB 3; Length 80;
Best Local Similarity 92.9%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TTGAGAACTTCGGG 18
Db 48 TTGAGAACTTCGGG 35

RESULT 19

US-10-071-411A-57
; Sequence 57, Application US/10071411A
; Patent No. 6797475
; GENERAL INFORMATION:
; APPLICANT: Glenn Barnes
; APPLICANT: Joanne Meyer
; TITLE OF INVENTION: Detection of Polymorphisms in the Human
; TITLE OF INVENTION: 5-lipoxygenase Gene
; FILE REFERENCE: MRI-021
; CURRENT APPLICATION NUMBER: US/10/071,411A
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/267,515
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/314,248
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-071-411A-57

Query Match 67.8%; Score 12.2; DB 3; Length 20;
Best Local Similarity 82.4%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTCGGG 18
Db 3 GCACGTGAGAACTTCGGG 19

RESULT 20

US-09-396-196G-26393/c
; Sequence 26393, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26393
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-26393

Query Match 67.8%; Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTTCGG 17
Db 20 TGCCTTGAGAACTTCGG 4

RESULT 21

US-09-396-196G-28314
; Sequence 28314, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28314
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-28314

Query Match 67.8%; Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTCGGG 18
Db 9 GCCGTGAGAACTTCGGG 25

RESULT 22

US-09-396-196G-28315
; Sequence 28315, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28315
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-28315

Query Match 67.8%; Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCCTTGAGAACTTCGGG 18
Db 7 GCCGTGAGAACTTCGGG 23

RESULT 23

US-09-396-196G-28317
; Sequence 28317, Application US/09396196G

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:25:53 ; Search time 984.737 Seconds
(without alignments)
855.220 Million cell updates/sec

Title: US-10-655-801-21
Perfect score: 18
Sequence: 1 tgccttgagaacttgggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 512758

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_hic: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_ges1: *
10: gb_ges2: *
11: gb_ges3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.2	73.3	79	9	AZ386276 LM0145109
2	13	72.2	50	1	AU108006
3	13	72.2	57	9	AZ308357
4	12.8	71.1	52	9	BZ354347 SALK_1248
5	12.8	71.1	57	4	AK203902 Mus muscu
6	12.8	71.1	61	1	AA128432 zn87h02.s
7	12.8	71.1	61	2	BG314971 OP3.0.5.H
8	12.8	71.1	63	10	BX892304
9	12.8	71.1	65	10	CL212445
10	12.8	71.1	66	3	BM284500
11	12.8	71.1	66	3	BM517906
12	12.8	71.1	80	11	CR397183
13	12.4	68.9	30	9	CC883430
14	12.4	68.9	33	9	BZ664879
15	12.4	68.9	52	9	BH790794
16	12.4	68.9	64	1	AA829832
17	12.4	68.9	65	6	CD909034
18	12.4	68.9	73	9	BZ381796
19	12.4	68.9	78	8	DR026237
20	12.2	67.8	49	1	AI528848
21	12.2	67.8	49	1	AA561711
22	12.2	67.8	54	11	CR022666 Reverse s

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c 96 11.2 62.2 51 8 DN603727 ACAC-aabs
97 11.2 62.2 55 9 CC887614 SALK_1504
98 11.2 62.2 57 5 BX723374 BX723374
99 11.2 62.2 58 1 AA935194 ny39b06.s
c 100 11.2 62.2 59 3 BM176238 T9ESTzby2

ALIGNMENTS

RESULT 1
AZ386276 79 bp DNA linear GSS 02-OCT-2000
LOCUS
DEFINITION
IM0145109F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0145109 F, genomic survey sequence.
ACCESSION
AZ386276
VERSION
AZ386276.1 GI:10499976
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 79)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Kelly,M., Rose,K., Rose,K., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0145 row: I column: 09
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 79.
FEATURES
source
Location/Qualifiers
1..79
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0145109"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

```

ORIGIN
Query Match 73.3%; Score 13.2; DB 9; Length 79;
Best Local Similarity 83.3%; Pred. No. 4.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTTCGGG 18
|||||
Db 29 TGCAGGAGAACTTCGGG 46

RESULT 2
AZ308357 57 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION
IM0011E16F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0011E16 F, genomic survey sequence.
ACCESSION
AZ308357
VERSION
AZ308357.1 GI:10348269
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 57)

FEATURES
source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="HEP16515"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 72.2%; Score 13; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCCTTGAGAACTT 14
|||||
Db 14 GCCTTGAGAACTT 26

RESULT 3
AZ308357 57 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION
IM0011E16F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0011E16 F, genomic survey sequence.
ACCESSION
AZ308357
VERSION
AZ308357.1 GI:10348269
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 57)

```

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0011 row: E column: 16
Seq primer: CGTTGTAAACGACGGCCACT
Class: plasmid ends
High quality sequence stop: 57.

FEATURES
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1. .57
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0011E16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 72.2%; Score 13; DB 9; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 TGCCTTGAGAACT 13
|||||
27 TGCCTTGAGAACT 39

Db
BZ354347 52 bp DNA linear GSS 14-NOV-2002
SALK_124807.28.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_124807.28.30.x, genomic survey sequence.

ACCESSION
BZ354347
VERSION
BZ354347.1 GI:24945209
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

REFERENCE
AUTHORS
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.

TITLE
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL
Unpublished (2001)

COMMENT
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@alk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At5g07170.
Class: TDNA tagged.

FEATURES
source
1. .52
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_124807.28.30.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 71.1%; Score 12.8; DB 9; Length 52;
Best Local Similarity 87.5%; Pred. No. 6.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
1 TGCCTTGAGAACTTCG 16
|||||
24 TCCCTTGAGAAATTCG 39

Db
AK203902 57 bp mRNA linear HTC 23-NOV-2004
Mus musculus cDNA, clone: Y1C0146J21, strand: plus,
reference: ENSEMBL: Mouse-Transcript-ENST: ENSMUST00000067124, based on BLAT search.

RESULT 5
AK203902/c
LOCUS
DEFINITION
Mus musculus (house mouse)
ACCESSION
AK203902.1 GI:56028079
VERSION
AK203902.1
KEYWORDS
HTC; ASSETS.
SOURCE
Mus musculus
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Watahiki, A., Waki, K., Hayatsu, N., Shiraki, T., Kondo, S., Nakamura, M., Sasaki, D., Arakawa, T., Kawai, J., Harbers, M., Hayashizaki, Y. and Carninci, P.

TITLE
Libraries enriched for alternatively spliced exons reveal splicing patterns in melanocytes and melanomas

JOURNAL
Nat. Methods 1, 233-239 (2004)

REFERENCE
AUTHORS
Arakawa, T., Carninci, P., Fukuda, S., Harbers, M., Hayatsu, N., Hori, F., Imotani, K., Kawai, J., Kondo, S., Murata, M., Nakamura, M., Nomura, K., Ohno, M., Sasaki, D., Shiraki, T., Waki, K., Watahiki, A. and Hayashizaki, Y.

TITLE
Direct Submission

JOURNAL
Submitted (15-SEP-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 52)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@alk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At5g07170.
Class: TDNA tagged.

FEATURES
source
1. .52
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_124807.28.30.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 71.1%; Score 12.8; DB 9; Length 52;
Best Local Similarity 87.5%; Pred. No. 6.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
1 TGCCTTGAGAACTTCG 16
|||||
24 TCCCTTGAGAAATTCG 39

Db
AK203902 57 bp mRNA linear HTC 23-NOV-2004
Mus musculus cDNA, clone: Y1C0146J21, strand: plus,
reference: ENSEMBL: Mouse-Transcript-ENST: ENSMUST00000067124, based on BLAT search.

RESULT 5
AK203902/c
LOCUS
DEFINITION
Mus musculus (house mouse)
ACCESSION
AK203902.1 GI:56028079
VERSION
AK203902.1
KEYWORDS
HTC; ASSETS.
SOURCE
Mus musculus
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Watahiki, A., Waki, K., Hayatsu, N., Shiraki, T., Kondo, S., Nakamura, M., Sasaki, D., Arakawa, T., Kawai, J., Harbers, M., Hayashizaki, Y. and Carninci, P.

TITLE
Libraries enriched for alternatively spliced exons reveal splicing patterns in melanocytes and melanomas

JOURNAL
Nat. Methods 1, 233-239 (2004)

REFERENCE
AUTHORS
Arakawa, T., Carninci, P., Fukuda, S., Harbers, M., Hayatsu, N., Hori, F., Imotani, K., Kawai, J., Kondo, S., Murata, M., Nakamura, M., Nomura, K., Ohno, M., Sasaki, D., Shiraki, T., Waki, K., Watahiki, A. and Hayashizaki, Y.

TITLE
Direct Submission

JOURNAL
Submitted (15-SEP-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
Alternative Splicing Libraries (ASLs) are prepared by: Preparing of single-stranded DNA using a RNA template from full length cDNA libraries, hybridizing of single-stranded DNAs, removing of remaining single-stranded DNA, digesting of regions comprising double-stranded DNA by a set of 4 bp-cutters, capturing of DNA hybrids with loop structures (alternative spliced exon), ligating of Y-shaped primers to isolated DNA hybrids with loop structures, PCR amplification of ligation products and their cloning into pPLCI vector. (Reference).

FEATURES

source

1..57
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="Y1G0146J21"
/cell_line="mixture of B16-F10Y and melan-c"
/cell_type="mixture of melanoma cell and melanocyte cell"
/clone_lib="Alternative Splicing Library Li"
/note="strand:plus, reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST0000067124, based on BLAT search"

ORIGIN

Query Match 71.1%; Score 12.8; DB 4; Length 57;
Best Local Similarity 87.5%; Pred. No. 6.3e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCCTTGAGAACTTCGG 17
||||| |||||
Db 40 GCCTTGAGCTCTTCGG 25

RESULT 6
AA128432
LOCUS AA128432 61 bp mRNA linear EST 01-AUG-1997
DEFINITION z87h02.61 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565203 3' similar to SW:RL29 HUMAN P47914 60S RIBOSOMAL PROTEIN L29. [1]; mRNA sequence.

ACCESSION AA128432
VERSION AA128432.1 GI:1689766
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 61)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.

TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
PUBMED 8889549

COMMENT Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Insert Length: 534 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

1..61
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:4594268"
/db_xref="taxon:9606"
/clone="IMAGE:565203"
/tissue_type="lung carcinoma"
/cell_line="NCI-H69"
/dev_stage="cell line NCI-H69"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene lung carcinoma 937218"
/notes="Organ: lung; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: oligo dt. Small cell carcinoma cell line NCI-H69. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN

Query Match 71.1%; Score 12.8; DB 1; Length 61;
Best Local Similarity 87.5%; Pred. No. 6.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCCTTGAGAACTTCGG 17
||||| |||||
Db 42 GCCTTGATTAACCTCGG 57

RESULT 7
BG314971/c
LOCUS BG314971 61 bp mRNA linear EST 28-FEB-2002
DEFINITION OP3.0.5 Human THP1 cell line library Homo sapiens cDNA, mRNA sequence.

ACCESSION BG314971
VERSION BG314971.1 GI:18997843
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 61)
AUTHORS Andersson, T., Borang, S., Larsson, M., Thelin, A., Ekstrand-Hammarstrom, B., Wirta, V., Wenborg, A., Lundberg, J. and Odeberg, J.

TITLE Identification of candidate genes in atherosclerosis - Virtual chip analysis in RDA based transcript profiling of monocyte/macrophage response to oxidised LDL
JOURNAL Unpublished (2001)
COMMENT Contact: Andersson Tove
Department of Biotechnology
KTH
Teknikringen 34, plan 6, 100 44 Stockholm, Sweden
Tel: +46 8 790 71 29
Fax: +46 8 245452
Email: tove@biotech.kth.se
POLYA=NO.

FEATURES
source 1..61
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="THP1"
/clone_lib="Human THP1 cell line library"
/note="Vector: pRIT28; Site 1: BamHI; Site 2: BamHI; Shotgun cloning of RDA difference products. Macrophage and foamcell libraries were submitted to successive rounds of subtractive hybridizations generating populations of gene fragments that are differentially expressed in macrophage to foam cell formation."

Query Match 71.1%; Score 12.8; DB 2; Length 61;

Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida;
Ascaridoidea; Ascarididae; Ascaris.
1 (bases 1 to 66)
McCarte J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
Wyllie, F., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tsagarishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCaun, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarte JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Claire Murphy, Brandi Chiapelli, and
Dr. James McCarte at Washington University, St. Louis. DNA
Sequencing by: Washington University Genome Sequencing Center
Seq primer: -40RP from Gibco.
Location/Qualifiers
FEATURES
source
1..66
/organism="Ascaris suum"
/mol_type="mRNA"
/db_xref="taxon:6253"
/sex="Male"
/tissue_type="Intestine"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Ascaris suum male gut SL1 TOPO v1 Murphy
Chiapelli McCarte"
/notes="Vector: pCRII-TOPO (Invitrogen); Site 1: EcoRI;
Site 2: EcoRI; The library was constructed by Claire
Murphy, Brandi Chiapelli, and Dr. James McCarte at
Washington University, St. Louis. Oligo(dT)-SL1 PCR based
library. Ascaris suum male intestine cDNA PCR products of
size >400 nucleotides containing SL1 on the 5' end and
oligo(dT) on the 3' end were non-directionally cloned
into pCRII-TOPO(Invitrogen) following the Topo TA cloning
protocol. Dissected nematode tissues were provided by Dr.
Alan Scott (ascott@jhph.edu) of the School of Public
Hygiene and Public Health at John Hopkins University in
Baltimore, MD"

Query Match 71.1%; Score 12.8; DB 3; Length 66;
Best Local Similarity 87.5%; Pred. No. 6.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTTCG 16
|||||
Db 43 TGCCTTGAGAACTTCG 28

RESULT 11
BM517906/c
LOCUS
DEFINITION
BM517906 66 bp mRNA linear EST 15-FEB-2002
McCarte Ascaris suum male head SL1 TOPO v1 Murphy Chiapelli
BM517906
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida;
Ascaridoidea; Ascarididae; Ascaris.
1 (bases 1 to 66)
McCarte J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
Wyllie, F., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,

Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida;
Ascaridoidea; Ascarididae; Ascaris.
1 (bases 1 to 66)
McCarte J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
Wyllie, F., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,

Tsagarishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCaun, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarte JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Claire Murphy, Brandi Chiapelli, and
Dr. James McCarte at Washington University, St. Louis. DNA
Sequencing by: Washington University Genome Sequencing Center
Seq primer: -40RP from Gibco.
Location/Qualifiers
FEATURES
source
1..66
/organism="Ascaris suum"
/mol_type="mRNA"
/db_xref="taxon:6253"
/sex="Male"
/tissue_type="Head"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Ascaris suum male head SL1 TOPO v1 Murphy
Chiapelli McCarte"
/notes="Vector: pCRII-TOPO (Invitrogen); Site 1: EcoRI;
Site 2: EcoRI; The library was constructed by Claire
Murphy, Brandi Chiapelli, and Dr. James McCarte at
Washington University, St. Louis. Oligo(dT)-SL1 PCR based
library. Ascaris suum male head cDNA PCR products of size
>400 nucleotides containing SL1 on the 5' end and
oligo(dT) on the 3' end were non-directionally cloned
into pCRII-TOPO(Invitrogen) following the Topo TA cloning
protocol. Dissected nematode tissues were provided by Dr.
Alan Scott (ascott@jhph.edu) of the School of Public
Hygiene and Public Health at John Hopkins University in
Baltimore, MD."

Query Match 71.1%; Score 12.8; DB 3; Length 66;
Best Local Similarity 87.5%; Pred. No. 6.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTTCG 16
|||||
Db 43 TGCCTTGAGAACTTCG 28

RESULT 12
CR397183
LOCUS
DEFINITION
CR397183 80 bp DNA linear GSS 02-MAY-2004
Arabidopsis thaliana T-DNA flanking sequence GK-414H01-026070,
genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weissshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
12874060
REFERENCE
2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
JOURNAL
COMMENT

Weishaar, B.
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
 flanking sequence tag-based reverse genetics
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 14756321
 Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
 Weishaar, B.
 High-throughput generation of sequence indexes from T-DNA
 mutagenized Arabidopsis thaliana lines
 Biotechniques 35 (6), 1164-1168 (2003)
 14682050
 4 (bases 1 to 80)
 Strizhov, N., Rosso, M.G., Li, Y. and Weishaar, B.
 Direct Submission
 Submitted (01-MAY-2004) Weishaar B., Max-Planck-Institut fuer
 Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence has been recovered from the left border of the T-DNA.
 It indicates an insertion close to or within gene At3g22690.
 Details on the protocols used for generation of the sequence are
 described in References 1-3. The sequences are generated at the MPI
 for Plant Breeding Research in the context of the GABI-Kat project.
 GABI-Kat is part of the German Plant Genomics program designated
 'GABI'. Information on line availability can be found at:
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES **source**

1. .80
 Location/Qualifiers
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /notes="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector pAC161 (GenBank accession number: AJ537514). The
 lines contain one or more T-DNA insertions. The DNA
 fragment(s) resulting from the PCR were directly sequenced
 to determine the genomic sequence flanking the insertion.
 T-DNA derived sequences were removed."

ORIGIN

Query Match 71.1%; Score 12.8; DB 11; Length 80;
 Best Local Similarity 87.5%; Pred. No. 6.7e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 CCTTGAGACTTCGGG 18
 Db 21 CTTTGAGACTTCGAG 36

RESULT 13
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CC883430
 SALK_094253.25.20.x Arabidopsis thaliana T-DNA insertion lines
 Arabidopsis thaliana genomic clone SALK_094253.25.20.x, genomic
 survey sequence.
 CC883430
 CC883430.1 GI:33359786
 GSS.
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 30)
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
 Shinn, P., Zimmerman, J. and Ecker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker

FEATURES **source**

1. .30
 Location/Qualifiers
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /notes="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more T-DNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 68.9%; Score 12.4; DB 9; Length 30;
 Best Local Similarity 92.9%; Pred. No. 9.4e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCCTTGAGACTT 14
 Db 23 TGCCTTGAGACTT 10

RESULT 14 **LOCUS** **DEFINITION**

BZ664879
 SALK_110222.24.20.x Arabidopsis thaliana T-DNA insertion lines
 Arabidopsis thaliana genomic clone SALK_110222.24.20.x, genomic
 survey sequence.
 BZ664879
 BZ664879.1 GI:28181941
 GSS.
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 33)
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
 Shinn, P., Zimmerman, J. and Ecker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker

TITLE **JOURNAL** **COMMENT**

The Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 T-DNA.
 Class: T-DNA tagged.
 Location/Qualifiers
 1. .33
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"

FEATURES **source**

1. .33
 Location/Qualifiers
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"

Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 T-DNA. This sequence lies within an annotated exon of At3g51570.
 Class: T-DNA tagged.

Location/Qualifiers
 1. .30
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /notes="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more T-DNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

Query Match 68.9%; Score 12.4; DB 9; Length 30;
 Best Local Similarity 92.9%; Pred. No. 9.4e+04;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCCTTGAGACTT 14
 Db 23 TGCCTTGAGACTT 10

RESULT 14 **LOCUS** **DEFINITION**

BZ664879
 SALK_110222.24.20.x Arabidopsis thaliana T-DNA insertion lines
 Arabidopsis thaliana genomic clone SALK_110222.24.20.x, genomic
 survey sequence.
 BZ664879
 BZ664879.1 GI:28181941
 GSS.
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 33)
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
 Shinn, P., Zimmerman, J. and Ecker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker

TITLE **JOURNAL** **COMMENT**

The Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 T-DNA.
 Class: T-DNA tagged.
 Location/Qualifiers
 1. .33
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"

FEATURES **source**

1. .33
 Location/Qualifiers
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 68.9%; Score 12.4; DB 9; Length 33;
Best Local Similarity 92.9%; Pred. No. 9.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TTGAGAACTTCGGG 18
|||||

Db 5 TTAGAACTTCGGG 18
|||||

RESULT 15

BH790794

LOCUS

DEFINITION SALK_057921.45.15.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_057921.45.15.x, genomic survey sequence.

ACCESSION BH790794

VERSION 1

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 52)

REFERENCE

AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,

Shinn, P., Zimmerman, J., and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

CONTACT: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of Atlg20850.

Class: TDNA tagged.

FEATURES

Location/Qualifiers

1..52

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_057921.45.15.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 68.9%; Score 12.4; DB 9; Length 52;

Best Local Similarity 92.9%; Pred. No. 1e+05;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCTTGAGAACTTCG 16
|||||

Db 3 CCTTGAGAACTTCG 16
|||||

RESULT 16

AA829832/c

LOCUS

DEFINITION

od40c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1370400 3',

mRNA sequence.

ACCESSION AA829832

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 64)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,

Ph.D., Gerald Marti, M.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 957 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 53.

Location/Qualifiers

1..64

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1370400"

/tissue_type="germinal center B cell"

/lab_host="DH10B"

/clone_lib="NCI CGAP GCB1"

/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was prepared from human tonsillar cells enriched for

germinal center B cells by flow sorting (CD20+, IgD-),

provided by Dr. Louis M. Staudt (NCI), Dr. David Allman

(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was

primed with a Not I - oligo(dT) primer

[5'-TGTTACCAATCTGAAGTGGAGCGCGCTCATTTTTTTTTTTT-3'

]. Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 68.9%; Score 12.4; DB 1; Length 64;

Best Local Similarity 92.9%; Pred. No. 1.1e+05;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCCTTGAGAACTTC 15
|||||

Db 58 GCCTTGAGAACTTC 45
|||||

RESULT 17

CD909034

LOCUS

DEFINITION

G468.111J08F010817 G468 Triticum aestivum cDNA clone G468111J08,

mRNA sequence.

ACCESSION CD909034

VERSION

KEYWORDS

SOURCE
ORGANISM
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 65)
AUTHORS
Genoplante.
TITLE
Genoplante, a major partnership french program in plant genomics
JOURNAL
Unpublished (2003)
COMMENT
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.

FEATURES
source
1..65
Location/Qualifiers
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="recital"
/db_xref="taxon:4565"
/clone="G46811J08"
/tissue_type="grain (468 degrees per day after pollination)"
/clone_lib="G468"

ORIGIN
Query Match 68.9%; Score 12.4; DB 6; Length 65;
Best Local Similarity 92.9%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TTGAGAACTTCGGG 18
|||||
DB 43 TTGAGTACTTCGGG 56
|||||

RESULT 18
BZ381796
LOCUS
DEFINITION
SALK_117315.18.95.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_117315.18.95.n, genomic survey sequence.
ACCESSION
BZ381796
VERSION
BZ381796.1 GI:25476104
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 73)
AUTHORS
Alonso,J.M., Leisese,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL
Unpublished (2001)
COMMENT
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..73
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"

FEATURES
source
1..73
Location/Qualifiers
/organism="Fragilariopsis cylindrus"
/mol_type="mRNA"
/db_xref="taxon:186039"
/clone="FCYLESTA35B04.s1"
/clone_lib="F. cylindrus osmotic stress library"
/note="Samples for total RNA isolation were taken continuous for 5 days after a salt shock treatment increasing salinity from 34 to 60 PSU. Total RNA extraktion was performed with RNeaqueous (Ambion) and mRNA purification with polyA Purist (Ambion). Further steps were carried out as described in the Cloneminer Kit. cDNA size fractionation was carried out with CHROMA Spin-400 columns and additionally on a gel."

ORIGIN
Query Match 68.9%; Score 12.4; DB 8; Length 78;
Best Local Similarity 92.9%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTT 14

ORIGIN
Query Match 68.9%; Score 12.4; DB 9; Length 73;
Best Local Similarity 92.9%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCTTGAGAACTTCG 16
|||||
DB 41 CCTTGAGAACTTTG 54
|||||

RESULT 19
DR026237/c
LOCUS
DEFINITION
Osm000105 F. cylindrus osmotic stress library Fragilariopsis cylindrus cDNA clone FCyleSTA35B04.s1, mRNA sequence.
ACCESSION
DR026237
VERSION
DR026237.1 GI:66748600
KEYWORDS
EST
SOURCE
Fragilariopsis cylindrus
Fragilariopsis cylindrus
Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae; Bacillariophycidae; Bacillariales; Bacillariaceae; Fragilariopsis.
REFERENCE
1 (bases 1 to 78)
AUTHORS
Krell,A. and Gloeckner,G.
TITLE
Analysis of an osmotic stress induced cDNA library of the psychrophilic diatom Fragilariopsis cylindrus
JOURNAL
Unpublished (2004)
COMMENT
Contact: Krell, Andreas; Gloeckner, Gernot
Biological Oceanography, Sea Ice Research; Genome Analysis
Alfred-Wegner-Institute for Polar and Marine Research; Institute for Molecular Biotechnology
Am Handelshafen 12, D-27570 Bremerhaven, Germany; Beutenbergstr. 11, D-07745 Jena, Germany
Tel: ++49 471 48311812; ++49 3641 656440
Fax: ++49 471 48311425; ++49 3641 656255
Email: akrell@wi-bremerhaven.de; gernot@imb-jena.de
PCR Primers
FORWARD: 5'M13
BACKWARD: 3'M13
Seq primer: 5'GTAAACGACGGCCAG 3'.
Location/Qualifiers
1..78
/organism="Fragilariopsis cylindrus"
/mol_type="mRNA"
/db_xref="taxon:186039"
/clone="FCYLESTA35B04.s1"
/clone_lib="F. cylindrus osmotic stress library"
/note="Samples for total RNA isolation were taken continuous for 5 days after a salt shock treatment increasing salinity from 34 to 60 PSU. Total RNA extraktion was performed with RNeaqueous (Ambion) and mRNA purification with polyA Purist (Ambion). Further steps were carried out as described in the Cloneminer Kit. cDNA size fractionation was carried out with CHROMA Spin-400 columns and additionally on a gel."

FEATURES
source
1..78
Location/Qualifiers
/organism="Fragilariopsis cylindrus"
/mol_type="mRNA"
/db_xref="taxon:186039"
/clone="FCYLESTA35B04.s1"
/clone_lib="F. cylindrus osmotic stress library"
/note="Samples for total RNA isolation were taken continuous for 5 days after a salt shock treatment increasing salinity from 34 to 60 PSU. Total RNA extraktion was performed with RNeaqueous (Ambion) and mRNA purification with polyA Purist (Ambion). Further steps were carried out as described in the Cloneminer Kit. cDNA size fractionation was carried out with CHROMA Spin-400 columns and additionally on a gel."

ORIGIN
Query Match 68.9%; Score 12.4; DB 8; Length 78;
Best Local Similarity 92.9%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCTTGAGAACTT 14

```

Db          69  TGTCTTGAGAACTT 56
|| |||||
|| |||||

RESULT 20
AI528848
LOCUS
DEFINITION
    ma21h05.x1 Stragatene mouse skin (#937313) Mus musculus cDNA clone
    IMAGE:607641 3' similar to SW:SPCO_MOUSE Q62261 SPECTRIN BETA
CHAIN, BRAIN ; mRNA sequence.
ACCESSION
AI528848
VERSION
AI528848.1 GI:4442983
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 49)
REFERENCE
    Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
    Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
    Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
    Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
    Waterston, R. and Wilson, R.
    The WashU-NCI Mouse EST Project 1999
    Unpublished (1999)
    Contact: Marra M/WashU-NCI Mouse EST Project 1999
    Washington University School of Medicine
    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
    Tel: 314 286 1800
    Fax: 314 286 1810
    Email: mouseest@watson.wustl.edu
    This clone is available royalty-free through LNL ; contact the
    IMAGE Consortium (info@image.llnl.gov) for further information.
    Trace considered overall poor quality
    Possible reversed clone: similarity on wrong strand
    High quality sequence stop: 1.
FEATURES
    source
    1..49
    /organism="Mus musculus"
    /mol_type="mRNA"
    /strain="C57BL/6"
    /db_xref="taxon:10090"
    /clone="IMAGE:607641"
    /sex="females"
    /tissue_type="whole skin"
    /dev_stage="11 weeks old"
    /lab_host="SOLR (kanamycin resistant)"
    /clone_lib="Stratagene mouse skin (#937313)"
    /note="Organ: skin; Vector: pBluescript SK-; Site 1:
    EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
    Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
    Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
    adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor
    sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
ORIGIN
    Query Match 67.8%; Score 12.2; DB 1; Length 49;
    Best Local Similarity 82.4%; Pred. No. 1.3e+05;
    Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGCCTTGAGAACTTCGG 17
|| |||||
Db 27 TCCCTTGAGAACTGTGG 43

RESULT 21
AA561711
LOCUS
DEFINITION
    v135e04.r1 Stragatene mouse skin (#937313) Mus musculus cDNA clone
    IMAGE:974238 5' similar to SW:CPG1_RAT P10610 CYTOCHROME P450 IIG1
    ; mRNA sequence.
ACCESSION
AA561711

```

```

VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
REFERENCE
    1 (bases 1 to 49)
AUTHORS
    Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
    Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
    Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
    Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
    Waterston, R.
    The WashU-HMI Mouse EST Project
    Unpublished (1996)
    Contact: Marra M/Mouse EST Project
    WashU-HMI Mouse EST Project
    Washington University School of Medicine
    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
    Tel: 314 286 1800
    Fax: 314 286 1810
    Email: mouseest@watson.wustl.edu
    This clone is available royalty-free through LNL ; contact the
    IMAGE Consortium (info@image.llnl.gov) for further information.
    MGI:554966
    Possible reversed clone: similarity on wrong strand
    Seq primer: -28ml3 rev1 Et from Amersham
    High quality sequence stop: 1.
FEATURES
    Location/Qualifiers
    1..49
    /organism="Mus musculus"
    /mol_type="mRNA"
    /strain="C57BL/6"
    /db_xref="taxon:10090"
    /clone="IMAGE:974238"
    /sex="females"
    /tissue_type="whole skin"
    /dev_stage="11 weeks old"
    /lab_host="SOLR (kanamycin resistant)"
    /clone_lib="Stratagene mouse skin (#937313)"
    /note="Organ: skin; Vector: pBluescript SK-; Site 1:
    EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
    Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
    Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
    adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor
    sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
ORIGIN
    Query Match 67.8%; Score 12.2; DB 1; Length 49;
    Best Local Similarity 82.4%; Pred. No. 1.3e+05;
    Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCCTTGAGAACTTCGG 18
|| |||||
Db 26 GCCTTGAGAACTTCGG 42

RESULT 22
CR022666
LOCUS
DEFINITION
    Reverse strand read from insert in 5'HPRT insertion targeting and
    chromosome engineering clone MHPN414915, genomic survey sequence.
ACCESSION
CR022666
VERSION
CR022666.1 GI:49755721
KEYWORDS
GSS; genome survey sequence; MICR.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 54)
REFERENCE
    Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
    Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,

```

Rogers, J. and Bradley, A.
 Direct Submission
 Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. <http://www.sanger.ac.uk/MICER>
 Location/Qualifiers
 1..54
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHPN414g15"
 /clone_lib="MHPN"

ORIGIN
 Query Match 67.8%; Score 12.2; DB 11; Length 54;
 Best Local Similarity 82.4%; Pred. No. 1.3e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCCTTGAGAACTTCGG 17
 Db 30 TTCCTTGAGAACTTCGG 46

RESULT 23
 CW187237
 LOCUS 73 bp DNA linear GSS 30-OCT-2004
 DEFINITION 104_605_11166986_116_36720_007 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11166986, genomic survey sequence.
 ACCESSION CW187237
 VERSION CW187237.1 GI:54895565
 KEYWORDS GSS.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
 REFERENCE 1 (bases 1 to 73)
 AUTHORS Jones, J.A., Budman, M.A., Nunberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Hogleman, H., Roe, B.A., Wiley, G., Korf, I.F., Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddloeh, J.A. and Martienssen, R.A.
 SORGHUM genome sequencing by methylation filtration
 PLoS Biol. 3 (1), e13 (2005)
 15660154
 CONTACT: Bedell JA
 Orion Genomics, LLC
 4041 Forest Park Ave, St. Louis, MO 63108, USA
 Tel: 314 615 6979
 Fax: 314 615 5975
 Email: jbedell@oriongenomics.com
 Plate: 605 row: j column: 02
 Seq primer: T3 Reverse
 Class: methylation filtered
 High quality sequence scop: 73.
 Location/Qualifiers
 1..73
 /organism="Sorghum bicolor"
 /mol_type="genomic DNA"
 /cultivar="Atx623"
 /db_xref="taxon:4558"
 /clone="11166986"
 /clone_lib="Sorghum methylation filtered library (LibID: 104)"
 /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

ORIGIN
 Query Match 67.8%; Score 12.2; DB 10; Length 73;

Best Local Similarity 82.4%; Pred. No. 1.4e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGCCCTTGAGAACTTCGG 17
 Db 41 TGCCCTTAGAATGTCGG 57

RESULT 24
 BX949767
 LOCUS 48 bp DNA linear GSS 05-APR-2004
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-803A08-023416, genomic survey sequence.
 ACCESSION BX949767
 VERSION BX949767.1 GI:42599453
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 REFERENCE 1
 AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
 Bioinformatics 19 (11), 1441-1442 (2003)
 12874060
 REFERENCE 2
 AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 14756321
 REFERENCE 3
 AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weisshaar, B.
 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
 Biotechniques 35 (6), 1164-1168 (2003)
 14682050
 REFERENCE 4 (bases 1 to 48)
 AUTHORS Strizhov, N., Rosso, M.G., Li, Y. and Weisshaar, B.
 Direct Submission
 Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At5g49650. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.
 Location/Qualifiers
 1..48
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="GK-803A08-023416"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC106 (GenBank accession number: AJ537513). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

FEATURES
 source
 ORIGIN
 Query Match 66.7%; Score 12; DB 10; Length 48;

Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTTGAGAACTTC 15
|||||
Db 17 CTTGAGAACTTC 28

RESULT 25
CN544831/c
LOCUS
DEFINITION
EST0003 Apple developing fruit differentially expressed cDNA
library Malus x domestica cDNA 5' similar to drought-stressed
related, mRNA sequence.

ACCESSION
CN544831
VERSION
CN544831.1 GI:46872987
KEYWORDS
EST.
SOURCE
Malus x domestica

ORGANISM
Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE
AUTHORS
Lin, S.F., Coleman, G.D. and Walsh, C.S.
TITLE
Transcript profiling the mechanism of transition from maturation to
ripening of 'Gala' and 'Fuji' apples
JOURNAL
Unpublished (2004)

COMMENT
Contact: Lin, Shu-fei
Department of Natural Resource Sciences and Landscape Architecture
University of Maryland College Park
2102 Plant Sciences Building, College Park, MD 20742, USA
Tel: 301 405 4367
Fax: 301 314 9308
Email: shufei@wam.umd.edu
CDNA-AFLP

Seq primer: M13-21
High quality sequence stop: 70

POLYA=No.

FEATURES
source Location/Qualifiers

1..70
/organism="Malus x domestica"
/mol_type="mRNA"
/cultivar="Gala"
/db_xref="taxon:3750"
/tissue_type="Hypanthium tissue"
/dev_stage="immature"
/clone_lib="Apple developing fruit differentially
expressed cDNA library"

ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTTGAGAACTTC 15
|||||
Db 40 CTTGAGAACTTC 29

Search completed: March 3, 2006, 11:01:35
Job time : 990.737 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:16:16 ; Search time 376.932 Seconds
(without alignments)
2714.499 Million cell updates/sec

Title: US-10-655-801-22

Perfect score: 18
Sequence: 1 tgcacttatctggatt 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5893141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2389942

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

GenEmbl.*
1: gb.ba.*
2: gb.in.*
3: gb.env.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pr.*
9: gb.ro.*
10: gb.sts.*
11: gb.sy.*
12: gb.un.*
13: gb.vi.*
14: gb.htg.*
15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.4	74.4	46	8	HSLAS73A
2	13.4	74.4	60	6	CQ542438
3	13.2	73.3	21	6	AX837834
4	13.2	73.3	26	6	A21788
5	13.2	73.3	48	6	AX925501
6	13.2	73.3	48	6	AX925502
7	13.2	73.3	65	6	CQ555999
8	13.2	73.3	77	6	CQ742818
9	13.2	73.3	80	10	BX294558
10	13	72.2	20	6	CQ945532
11	12.8	71.1	19	6	AR573430
12	12.8	71.1	19	6	AR573431
13	12.8	71.1	19	6	AX131540
14	12.8	71.1	19	6	AX131541
15	12.8	71.1	24	6	AX321460
16	12.8	71.1	27	6	AR448509
17	12.8	71.1	27	6	AX255427
18	12.8	71.1	47	6	AR291139

c	19	12.8	71.1	51	6	AX427630	Sequence
c	20	12.8	71.1	54	6	AX427632	Sequence
c	21	12.8	71.1	65	6	CQ534533	Sequence
c	22	12.8	71.1	65	6	AX484056	Sequence
c	23	12.4	68.9	15	6	A11087	Oligonucleo
c	24	12.4	68.9	15	6	AR340899	Sequence
c	25	12.4	68.9	15	6	AR362712	Sequence
c	26	12.4	68.9	21	6	CQ868436	Sequence
c	27	12.4	68.9	21	6	CQ955649	Sequence
c	28	12.4	68.9	23	6	CS114991	Sequence
c	29	12.4	68.9	25	6	AX614147	Sequence
c	30	12.4	68.9	30	6	AX207312	Sequence
c	31	12.4	68.9	41	6	AX518625	Sequence
c	32	12.4	68.9	41	6	AX518626	Sequence
c	33	12.4	68.9	42	6	AR055004	Sequence
c	34	12.4	68.9	42	6	AR156253	Sequence
c	35	12.4	68.9	42	6	AX343177	Sequence
c	36	12.4	68.9	47	6	E15363	Oligonucleo
c	37	12.4	68.9	47	6	AR289908	Sequence
c	38	12.4	68.9	47	6	AR289924	Sequence
c	39	12.4	68.9	60	6	CQ784697	Sequence
c	40	12.4	68.9	60	6	AX496193	Sequence
c	41	12.4	68.9	63	6	BD035124	Sequence
c	42	12.4	68.9	63	6	AX899591	Sequence
c	43	12.4	68.9	65	6	CQ531358	Sequence
c	44	12.2	67.8	21	6	A95016	Sequence 22
c	45	12.2	67.8	21	6	E38368	Binding par
c	46	12.2	67.8	21	6	E39012	Nucleic aci
c	47	12.2	67.8	21	6	AX022660	Sequence
c	48	12.2	67.8	25	6	BD245513	Developme
c	49	12.2	67.8	25	6	CS117930	Sequence
c	50	12.2	67.8	30	6	AR107083	Sequence
c	51	12.2	67.8	30	6	AR107088	Sequence
c	52	12.2	67.8	30	6	AR118363	Sequence
c	53	12.2	67.8	30	6	AR118368	Sequence
c	54	12.2	67.8	30	6	CQ874733	Sequence
c	55	12.2	67.8	30	6	CS020544	Sequence
c	56	12.2	67.8	30	6	CS020548	Sequence
c	57	12.2	67.8	30	6	CS070456	Sequence
c	58	12.2	67.8	30	6	CS070461	Sequence
c	59	12.2	67.8	30	6	CS103069	Sequence
c	60	12.2	67.8	30	6	AR302205	Sequence
c	61	12.2	67.8	30	6	AR302210	Sequence
c	62	12.2	67.8	30	6	AR308644	Sequence
c	63	12.2	67.8	30	6	AR308722	Sequence
c	64	12.2	67.8	30	6	AR633343	Sequence
c	65	12.2	67.8	30	6	AR633348	Sequence
c	66	12.2	67.8	30	6	AX813365	Sequence
c	67	12.2	67.8	30	6	AX813370	Sequence
c	68	12.2	67.8	30	15	AJ837777	Arabidops
c	69	12.2	67.8	31	6	BD136169	Vector . 9
c	70	12.2	67.8	31	6	AR635373	Sequence
c	71	12.2	67.8	31	6	AX002799	Sequence
c	72	12.2	67.8	31	6	AX149567	Sequence
c	73	12.2	67.8	34	6	AX577721	Sequence
c	74	12.2	67.8	37	6	AR591114	Sequence
c	75	12.2	67.8	37	6	AR591115	Sequence
c	76	12.2	67.8	37	6	AX280622	Sequence
c	77	12.2	67.8	37	6	AX280623	Sequence
c	78	12.2	67.8	41	6	AX516052	Sequence
c	79	12.2	67.8	41	6	AX517111	Sequence
c	80	12.2	67.8	41	6	AX517458	Sequence
c	81	12.2	67.8	41	6	AX519640	Sequence
c	82	12.2	67.8	47	6	AX066417	Sequence
c	83	12.2	67.8	49	6	AX066418	Sequence
c	84	12.2	67.8	50	6	AR032931	Sequence
c	85	12.2	67.8	50	6	I29671	Sequence 54
c	86	12.2	67.8	50	6	I91345	Sequence 54
c	87	12.2	67.8	50	6	AR209595	Sequence
c	88	12.2	67.8	50	6	AR646309	Sequence
c	89	12.2	67.8	51	10	BV183752	Sequence
c	90	12.2	67.8	53	6	AR355948	Sequence
c	91	12.2	67.8	53	6	AR537504	Sequence

C 92 12.2 67.8 65 6 AX483731 Sequence
 C 93 12 66.7 17 6 AX234635 Sequence
 C 94 11.8 65.6 17 6 AX722575 Sequence
 C 95 11.8 65.6 17 6 AX736854 Sequence
 C 96 11.8 65.6 20 6 122554 Sequence 42
 C 97 11.8 65.6 20 6 147379 Sequence 42
 C 98 11.8 65.6 21 6 A91087 Sequence 8
 C 99 11.8 65.6 21 6 CQ778220 Sequence
 C 100 11.8 65.6 21 6 AR530667 Sequence

ALIGNMENTS

RESULT 1
 HSLAS73A
 LOCUS HSLAS73A 46 bp DNA linear PRI 22-APR-1996
 DEFINITION H. sapiens DNA for loop attachment sequence (clone LAS73A).
 ACCESSION X91571
 VERSION X91571.1 GI:987929
 KEYWORDS loop attachment sequence.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 46)
 AUTHORS Jackson,D.A., Barlett,J. and Cook,P.R.
 TITLE Sequences attaching loops of nuclear and mitochondrial DNA to underlying structures in human cells: the role of transcription units
 JOURNAL Nucleic Acids Res. 24 (7), 1212-1219 (1996)
 PUBMED 8614821
 REFERENCE 2 (bases 1 to 46)
 AUTHORS Cook,P.R.
 TITLE Direct Submission
 JOURNAL Submitted (14-SEP-1995) P.R. Cook, Sir William Dunn School of Pathology, University of Oxford, South Parks Road, Oxford, OX1 3RE, UK

FEATURES

source 1..46
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="LAS73A"
 /cell_line="HeLa"
 /clone_lib="DNA loop attachment sequences (LAS)"
 misc_feature 1..46
 /note="DNA loop attachment site (LAS)"

ORIGIN

Query Match 74.4%; Score 13.4; DB 8; Length 46;
 Best Local Similarity 93.3%; Pred. No. 3.1e+04;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTCACTTCTCTGGA 15
 |||||
 Db 31 TGTCACTTCTCTGGA 45

RESULT 2
 CQ542438
 LOCUS CQ542438 60 bp DNA linear PAT 30-JAN-2004
 DEFINITION Sequence 12073 from Patent WO0210449.
 ACCESSION CQ542438
 VERSION CQ542438.1 GI:41508702
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE

1

AUTHORS Shohan,A., Wasserman,A., Mintz,E., Mintz,L. and Paigler,S.
 TITLE Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
 JOURNAL Patent: WO 0210449-A 12073 07-FEB-2002;
 Compugen Inc. (US)
 FEATURES Location/Qualifiers
 source 1..60
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 74.4%; Score 13.4; DB 6; Length 60;
 Best Local Similarity 93.3%; Pred. No. 3e+04; 1; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTCACTTCTCTGGA 15
 |||||
 Db 38 TGTCACTTCTCTGGA 52

RESULT 3

AX837834/c
 LOCUS AX837834 21 bp DNA linear PAT 15-DEC-2003
 DEFINITION Sequence 4958 from Patent EP1347046.
 ACCESSION AX837834
 VERSION AX837834.1 GI:39921526
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified sequences.

REFERENCE 1
 AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Yamachika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahara,K. and Masuho,Y.
 TITLE Full-length cDNA sequences
 JOURNAL Patent: EP 1347046-A 4958 24-SEP-2003;
 Research Association for Biotechnology (JP)

FEATURES

source 1..21
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"
 /note="Description of Artificial Sequence: an artificially synthesized primer se q"

ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 21;
 Best Local Similarity 83.3%; Pred. No. 4.2e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTCTCTGGA 18
 |||||
 Db 20 TGTCACTTCTCTGGA 3

RESULT 4

A21788
 LOCUS A21788 26 bp DNA linear PAT 22-AUG-1994
 DEFINITION SEQ ID NO: 4; Oligonucleotide.
 ACCESSION A21788
 VERSION A21788.1 GI:583664
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 26)

AUTHORS Novoa Perez,L.I., Machado Lahera,J.A., Fernandez Maso,J.R., Benitez Fuentes,J.V., Nardiandi Diaz,R.E., Rodriguez Reinoso,J.L., Estrada Garcia,M.P., Garcia Suarez,J. and Herrera Martinez,L.S.
 TITLE Method for the expression of heterologous proteins produced in fused form in E. coli, use thereof, expression vectors and

JOURNAL
 FEATURES
 source
 recombinant strains
 Patent: EP 0416673-A 4 13-MAR-1991;
 CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA
 Location/Qualifiers
 1. .26
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"

ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 26;
 Best Local Similarity 83.3%; Pred. No. 4.2e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
 ||||| ||||| ||||| ||
 Db 8 TATCAGTAGCTGGATT 25

RESULT 5

LOCUS AX925501/c 48 bp DNA linear PAT 19-DEC-2003
 DEFINITION Sequence 2 from Patent WO02068631.
 ACCESSION AX925501
 VERSION AX925501.1 GI:40243764
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

REFERENCE 1
 AUTHORS Shaw, K.J., Kenney, T. and Shimer, G.H.
 TITLE Plasmid for insertional mutagenesis in bacteria
 JOURNAL Patent: WO 02068631-A 2 06-SEP-2002;
 Genome Therapeutics Corporation (US)

FEATURES

1. .48
 Location/Qualifiers
 source
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Primer Sequence"

ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 48;
 Best Local Similarity 83.3%; Pred. No. 4e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
 ||||| ||||| ||||| ||
 Db 33 TGTCACTAACCTGGATT 16

RESULT 6

LOCUS AX925502 48 bp DNA linear PAT 19-DEC-2003
 DEFINITION Sequence 3 from Patent WO02068631.
 ACCESSION AX925502
 VERSION AX925502.1 GI:40243767
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

REFERENCE 1
 AUTHORS Shaw, K.J., Kenney, T. and Shimer, G.H.
 TITLE Plasmid for insertional mutagenesis in bacteria
 JOURNAL Patent: WO 02068631-A 3 06-SEP-2002;
 Genome Therapeutics Corporation (US)

FEATURES

1. .48
 Location/Qualifiers
 source
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Primer Sequence"

ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 48;
 Best Local Similarity 83.3%; Pred. No. 4e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
 ||||| ||||| ||||| ||
 Db 16 TGTCACTAACCTGGATT 33

RESULT 7

LOCUS CQ555999 65 bp DNA linear PAT 30-JAN-2004
 DEFINITION Sequence 25634 from Patent WO0210449.
 ACCESSION CQ555999
 VERSION CQ555999.1 GI:41522426
 KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE

1
 AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
 TITLE Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
 JOURNAL Patent: WO 0210449-A 25634 07-FEB-2002;
 Compugen Inc. (US)

FEATURES

1. .65
 Location/Qualifiers
 source
 /organism="Mus musculus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:10090"

ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 65;
 Best Local Similarity 83.3%; Pred. No. 3.9e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
 ||||| ||||| ||||| ||
 Db 32 TGTCACTATCTGGATT 49

RESULT 8

LOCUS CQ742818/c 77 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 28752 from Patent WO02068579.
 ACCESSION CQ742818
 VERSION CQ742818.1 GI:42354141
 KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

1
 AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
 TITLE Kits, such as nucleic acid arrays, comprising a majority of human exons or transcripts, for detecting expression and other uses thereof
 JOURNAL Patent: WO 02068579-A 28752 06-SEP-2002;
 PE Corporation (NY) (US)

FEATURES

1. .77
 Location/Qualifiers
 source
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 77;
 Best Local Similarity 83.3%; Pred. No. 3.9e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGATT 17
|||||
Db 3 GTCCTTAACTGGATT 18

RESULT 13
AX131540
LOCUS
DEFINITION
Sequence 2758 from Patent WO0130362.
ACCESSION
AX131540
VERSION
AX131540.1 GI:14137845
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
Robbins,J.M. and Tritz,R.
TITLE
Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL
Patent: WO 0130362-A 2758 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source
1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cyclin G1 ribozyme binding site"

Query Match 71.1%; Score 12.8; DB 6; Length 19;
Best Local Similarity 87.5%; Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGATT 17
|||||
Db 4 GTCCTTAACTGGATT 19

RESULT 14
AX131541
LOCUS
DEFINITION
Sequence 2759 from Patent WO0130362.
ACCESSION
AX131541
VERSION
AX131541.1 GI:14137846
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
Robbins,J.M. and Tritz,R.
TITLE
Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL
Patent: WO 0130362-A 2759 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source
1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cyclin G1 ribozyme binding site"

Query Match 71.1%; Score 12.8; DB 6; Length 19;
Best Local Similarity 87.5%; Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGATT 17
|||||

Db 3 GTCCTTAACTGGATT 18
|||||

RESULT 15
AX321460
LOCUS
DEFINITION
Sequence 10 from Patent WO0190413.
ACCESSION
AX321460
VERSION
AX321460.1 GI:17905447
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS
Rosell,R. and Monzo,M.
TITLE
Method and markers for prognosticating efficacy of anticancer agents
JOURNAL
Patent: WO 0190413-A 10 29-NOV-2001;
Bristol-Myers Squibb Co. (US)
FEATURES
source
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 71.1%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCACCTTATCTGGATT 18
|||||

Db 7 TAACTTACTGGATT 22
|||||

RESULT 16
AR448509/c
LOCUS
DEFINITION
Sequence 7 from patent US 6673567.
ACCESSION
AR448509
VERSION
AR448509.1 GI:42676997
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.

REFERENCE
AUTHORS
Sharpe,P.L. and Nagarajan,V.
TITLE
Method of determination of gene function
JOURNAL
Patent: US 6673567-A 7 06-JAN-2004;
E. I. du Pont de Nemours and Company; Wilmington, DE
FEATURES
source
1. .27
/organism="unknown"
/mol_type="genomic DNA"

Query Match 71.1%; Score 12.8; DB 6; Length 27;
Best Local Similarity 87.5%; Pred. No. 7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGAT 16
|||||

Db 18 TTTCACCTTATCTGGTT 3
|||||

RESULT 17
AX255427/c
LOCUS
DEFINITION
Sequence 7 from Patent WO0171040.
ACCESSION
AX255427
VERSION
AX255427.1 GI:16074601
KEYWORDS

Query Match 71.1%; Score 12.8; DB 6; Length 27;
Best Local Similarity 87.5%; Pred. No. 7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGAT 16
|||||

Db 18 TTTCACCTTATCTGGTT 3
|||||

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SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Sharpe,P.L., Cheng,O. and Nagarajan,V.
TITLE       Method for determination of gene function
JOURNAL     Patent: WO 0171040-A 7 27-SEP-2001;
            E.I. DUPONT DE NEMOURS AND COMPANY (US)
FEATURES   Location/Qualifiers
            source
            1..27
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="primer sequence"
ORIGIN
Query Match      71.1%; Score 12.8; DB 6; Length 27;
Best Local Similarity 87.5%; Pred. NO. 7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGTCACTTATCTGGAT 16
    |||||
Db 18 TTCACTTATCTGGTT 3

RESULT 18
AR291139/c
LOCUS      AR291139          47 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 2874 from patent US 6537751.
ACCESSION  AR291139
VERSION     AR291139.1 GI:31678423
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 47)
AUTHORS     Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE       Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
JOURNAL     Patent: US 6537751-A 2874 25-MAR-2003;
            Genset S.A.;
            FRX;
FEATURES   Location/Qualifiers
            source
            1..47
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN

Query Match      71.1%; Score 12.8; DB 6; Length 47;
Best Local Similarity 87.5%; Pred. NO. 6.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGTCACTTATCTGGAT 16
    |||||
Db 22 TATCACTTATCTGAAT 7

RESULT 19
AX427630/c
LOCUS      AX427630          51 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 15 from Patent EP1199365.
ACCESSION  AX427630
VERSION     AX427630.1 GI:21537750
KEYWORDS   .
SOURCE     Bacillus pumilus
            Bacillus pumilus
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
REFERENCE   1
AUTHORS     Xu,S.Y., Xiao,J.P. and Zhu,Z.
TITLE       Method for cloning and expression of BPMT restriction endonuclease
            in E. coli
JOURNAL     Patent: EP 1199365-A 15 24-APR-2002;
            NEW ENGLAND BIOLABS, INC. (US)

SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Sharpe,P.L., Cheng,O. and Nagarajan,V.
TITLE       Method for determination of gene function
JOURNAL     Patent: WO 0171040-A 7 27-SEP-2001;
            E.I. DUPONT DE NEMOURS AND COMPANY (US)
FEATURES   Location/Qualifiers
            source
            1..51
            /organism="Bacillus pumilus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:1408"
ORIGIN

Query Match      71.1%; Score 12.8; DB 6; Length 51;
Best Local Similarity 87.5%; Pred. NO. 6.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCACCTTATCTGGATTT 18
    |||||
Db 35 TCACCTTATATGCATTT 20

RESULT 20
AX427632/c
LOCUS      AX427632          54 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 17 from Patent EP1199365.
ACCESSION  AX427632
VERSION     AX427632.1 GI:21537752
KEYWORDS   .
SOURCE     Bacillus pumilus
            Bacillus pumilus
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
REFERENCE   1
AUTHORS     Xu,S.Y., Xiao,J.P. and Zhu,Z.
TITLE       Method for cloning and expression of BPMT restriction endonuclease
            in E. coli
JOURNAL     Patent: EP 1199365-A 17 24-APR-2002;
            NEW ENGLAND BIOLABS, INC. (US)
FEATURES   Location/Qualifiers
            source
            1..54
            /organism="Bacillus pumilus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:1408"
ORIGIN

Query Match      71.1%; Score 12.8; DB 6; Length 54;
Best Local Similarity 87.5%; Pred. NO. 6.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCACCTTATCTGGATTT 18
    |||||
Db 38 TCACCTTATATGCATTT 23

RESULT 21
CQ534533
LOCUS      CQ534533          65 bp      DNA      linear      PAT 30-JAN-2004
DEFINITION Sequence 4168 from Patent WO0210449.
ACCESSION  CQ534533
VERSION     CQ534533.1 GI:41500797
KEYWORDS   .
SOURCE     Rattus norvegicus (Norway rat)
            Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Rattus.
REFERENCE   1
AUTHORS     Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE       Oligonucleotide library for detecting rna transcripts and splice
            variants that populate a transcriptome
JOURNAL     Patent: WO 0210449-A 4168 07-FEB-2002;
            Compugen Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..65
            /organism="Rattus norvegicus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:10116"
ORIGIN

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Query Match      71.1%; Score 12.8; DB 6; Length 65;
Best Local Similarity 87.5%; Pred. No. 6.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCACCTTATCTGGATT 18
    ||||| ||||| |||||
Db 2 TCACCTGCTGGATT 17

RESULT 22
AX484056/c
LOCUS AX484056 65 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 1356 from Patent WO02053728.
ACCESSION AX484056
VERSION AX484056.1 GI:22318408
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Roemer T., Jiang B., Boone C., Bussey H. and Ohlisen K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 1996 11-JUL-2002;
Elitra Pharmaceuticals, Inc. (US)
FEATURES
source
Location/Qualifiers
1..65
/organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"

ORIGIN
Query Match      71.1%; Score 12.8; DB 6; Length 65;
Best Local Similarity 87.5%; Pred. No. 6.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGATT 17
    ||||| ||||| |||||
Db 48 GTCACCTTATCTGATT 33

RESULT 23
A11087
LOCUS A11087 15 bp DNA linear PAT 03-DEC-1993
DEFINITION Oligonucleotide U16.
ACCESSION A11087
VERSION A11087.1 GI:490937
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Ikehara, M. and Kida, M.
TITLE Synthetic gene for human lysozyme
JOURNAL Patent: EP 0181634-A 31 21-MAY-1986;
Takeda Chemical Industries, Ltd
FEATURES
source
Location/Qualifiers
1..15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match      68.9%; Score 12.4; DB 6; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTCACCTTATCTGG 14
    ||||| ||||| |||||
Db 1 TGTCACCTTATCTGG 14

RESULT 24
A11087
LOCUS A11087 15 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 46 from patent US 5182195.
ACCESSION A11087
VERSION A11087.1 GI:34423092
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Nakahama, K., Kaisho, Y. and Yoshimura, K.
TITLE Method for increasing gene expression using protease deficient
JOURNAL Patent: US 5182195-A 46 26-JAN-1993;
Takeda Chemical Industries, Ltd.; Osaka;
JPX;
FEATURES
source
Location/Qualifiers
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/organism="genomic DNA"
/mol_type="genomic DNA"

ORIGIN
Query Match      68.9%; Score 12.4; DB 6; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTCACCTTATCTGG 14
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Db 1 TGTCACCTTATCTGG 14

Search completed: March 3, 2006, 08:38:53
JOB time : 377.932 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:02:58 ; Search time 117.534 Seconds
(without alignments)
1020.680 Million cell updates/sec

Title: US-10-655-801-22

Perfect score: 18

Sequence: 1 tgcacttcttgattt 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4995997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 5180220

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

N_Geneseq_21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	100.0	18	AAH47978	Aah47978 Human ind
2	14	77.8	19	ADQ62106	Adq62106 Anti-NOS2
3	13.8	76.7	30	ADR16179	Adr16179 Versinia
4	13.4	74.4	25	ADP13976	Adp13976 Renal cel
5	13.4	74.4	25	ADP13977	Adp13977 Renal cel
6	13.4	74.4	41	ADL01630	Adl01630 Escherich
7	13.4	74.4	60	ABN39325	Abn39325 Human spl
8	13.2	73.3	21	ADM06273	Adm06273 Human PCR
9	13.2	73.3	45	AACB2169	AacB2169 Human ret
10	13.2	73.3	48	ABSS5303	Abss5303 PLAC prom
11	13.2	73.3	48	ABSS5302	Abss5302 Chloramph
12	13.2	73.3	65	ABNS52886	Abns52886 Mouse spl
13	13.2	73.3	75	ADP80938	Adp80938 Mouse Dna
14	13	72.2	20	ADU73604	Adu73604 Probe N-S
15	13	72.2	50	ADR70635	Adr70635 Exemplary
16	12.8	71.1	19	AAA85172	Aaa85172 Cyclin G1
17	12.8	71.1	19	AAA85173	Aaa85173 Cyclin G1
18	12.8	71.1	19	AAH60334	Aah60334 Cyclin G1
19	12.8	71.1	19	AAH60335	Aah60335 Cyclin G1

23	71.1	12.8	C 20	AAE82405	Aaf82405 Mealworm
24	71.1	12.8	21	AAE26335	Aad26335 Human bet
27	71.1	12.8	C 22	AAE13868	Aas13868 Tn5-based
41	71.1	12.8	C 23	ABZ48041	Abz48041 Human ATP
41	71.1	12.8	C 24	ABZ48040	Abz48040 Human ATP
47	71.1	12.8	C 25	AAZ68526	Aaz68526 Human map
50	71.1	12.8	C 26	AAZ03967	Abz03967 Human leu
51	71.1	12.8	C 27	AAK99735	Aak99735 Bpmi endo
51	71.1	12.8	C 28	ADU24034	Adu24034 PCR prime
54	71.1	12.8	C 29	AAK99737	Aak99737 Bpmi endo
54	71.1	12.8	C 30	ADU24038	Adu24038 Type IIG
54	71.1	12.8	C 31	ADU24036	Adu24036 Forward P
60	71.1	12.8	C 32	ADZ63509	Adz63509 Murine Ap
64	71.1	12.8	C 33	ADO05654	Ado05654 PCR ampli
64	71.1	12.8	C 34	ADO05653	Ado05653 PCR ampli
65	71.1	12.8	C 35	ABZ27409	Abz27409 Candida e
65	71.1	12.8	C 36	ABN31420	Abn31420 Rat splic
79	71.1	12.8	C 37	AAE11606	Aax11606 Human bia
17	68.9	12.4	C 38	ADX01097	Adx01097 Drug-resi
21	68.9	12.4	C 39	ADR70371	Adr70371 Polioviru
22	68.9	12.4	C 40	ADS19213	Adsl9213 Serine or
23	68.9	12.4	C 41	ABS98050	Abs98050 Human mul
23	68.9	12.4	C 42	ADM79746	Adm79746 Group B S
23	68.9	12.4	C 43	ADM79642	Adm79642 Group B S
30	68.9	12.4	C 44	AEA46753	Aea46753 FKPB51 SN
30	68.9	12.4	C 45	AAE14231	Aad14231 Synthetic
32	68.9	12.4	C 46	AAO6566	Aao6566 Mouse mic
32	68.9	12.4	C 47	ADM26071	Adm26071 Plant tri
42	68.9	12.4	C 48	AAE6880	Aat6880 Plasmid P
42	68.9	12.4	C 49	AAV64697	Aav64697 HIV anti-
42	68.9	12.4	C 50	AAH24709	Aah24709 Nucleotid
42	68.9	12.4	C 51	ACA74015	Acav74015 Hepatitis
47	68.9	12.4	C 52	AAV22795	Aav22795 Oligonucl
60	68.9	12.4	C 53	ABQ96308	Abq96308 Tumour su
60	68.9	12.4	C 54	ADK19630	Adk19630 Anti-M2-P
63	68.9	12.4	C 55	AAE11379	Aac11379 Human sec
65	68.9	12.4	C 56	ABN28245	Abn28245 Rat splic
21	67.8	12.2	C 57	AAE77905	Aax77905 Murine pl
21	67.8	12.2	C 58	AAE77884	Aax77884 Mouse pl6
21	67.8	12.2	C 59	AAE65146	Aae65146 Human lup
21	67.8	12.2	C 60	ADZ99147	Adz99147 Human NOT
22	67.8	12.2	C 61	ADG38398	Adg38398 PCR prime
23	67.8	12.2	C 62	ADB76941	Adb76941 Mouse CLC
23	67.8	12.2	C 63	ADB76939	Adb76939 Mouse CLC
23	67.8	12.2	C 64	ADI29527	Adi29527 Murine CL
23	67.8	12.2	C 65	ADI29529	Adi29529 Murine CL
23	67.8	12.2	C 66	ADJ34752	Adj34752 Mouse 2-
25	67.8	12.2	C 67	AAA68488	Aaa68488 Bacteriop
25	67.8	12.2	C 68	ACI09914	Act09914 Human mic
25	67.8	12.2	C 69	ACK28853	Ack28853 Human mic
25	67.8	12.2	C 70	ACI51041	Act51041 Human mic
27	67.8	12.2	C 71	ABZ80482	Abz80482 Human imm
30	67.8	12.2	C 72	AAZ08106	Aaz08106 3'UT-PCR
30	67.8	12.2	C 73	AAZ08111	Aaz08111 PCR prime
30	67.8	12.2	C 74	AAA30747	Aaa30747 Human GPC
30	67.8	12.2	C 75	AAA30668	Aaa30668 Human G p
30	67.8	12.2	C 76	AAE32187	Aaf32187 Human oes
30	67.8	12.2	C 77	AAE82810	Aac82810 Human ser
30	67.8	12.2	C 78	AAE82815	Aac82815 Human ser
30	67.8	12.2	C 79	ADC22639	Adc22639 Human G p
30	67.8	12.2	C 80	ADC22755	Adc22755 Human G p
30	67.8	12.2	C 81	ADH14228	Adh14228 Human GPC
30	67.8	12.2	C 82	ADH14112	Adh14112 Human ser
30	67.8	12.2	C 83	ADI24561	Adi24561 Human SHT
30	67.8	12.2	C 84	ADI24556	Adi24556 Human SHT
30	67.8	12.2	C 85	ADR99761	Adr99761 Nucleic a
30	67.8	12.2	C 86	ADX02766	Adx02766 Human 5-H
30	67.8	12.2	C 87	ADX02770	Adx02770 Human 5-H
31	67.8	12.2	C 88	AAV80316	Aav80316 Reverse p
31	67.8	12.2	C 89	AAE99722	Aae99722 PCR prime
33	67.8	12.2	C 90	ABA05757	Abao5757 Human NTF
34	67.8	12.2	C 91	ABZ59225	Abz59225 Gentamici
36	67.8	12.2	C 92	ADY01040	Ady01040 PCR prime

c 93 12.2 67.8 37 5 ABI97793 Abi97793 Non-endog
 94 12.2 67.8 37 5 ABI97794 Abi97794 Non-endog
 c 95 12.2 67.8 41 2 AAQ12334 Aaq12334 HPV exon-
 96 12.2 67.8 41 6 ABA05759 Abo05759 Human NTF
 97 12.2 67.8 41 6 ABA05760 Abo05760 Human NTF
 98 12.2 67.8 41 6 ABZ49055 Abz49055 Human ALD
 99 12.2 67.8 41 6 ABZ46525 Abz46525 Human ALD
 100 12.2 67.8 42 10 ABX93701 Abx93701 2C-methyl

ALIGNMENTS

RESULT 1
 AAH47978
 ID AAH47978 standard; DNA; 18 BP.
 AC AAH47978;
 XX
 XX
 DT 02-OCT-2001 (first entry)
 XX
 DE Human inducible NOS antisense oligonucleotide SEQ ID NO 22.
 XX
 KW Antisense oligonucleotide; inducible nitric oxide synthase; NOS;
 KW modulate expression; immunomodulator; antidiabetic; cardiovascular;
 KW cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;
 KW 2'-O-methoxyethyl; phosphorothioate; human; ss.
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH modified_base 1..18
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone, 5' and 3' four
 nucleotide 2'-MOE (2'-O-methoxyethyl) wings (the cytidine
 residues in the 2'-MOE wings are 5-methylcytidines) and a
 deoxy gap"
 XX
 XX WO200152902-A1.
 XX
 XX 26-JUL-2001.
 XX
 XX 15-JAN-2001; 2001WO-US001381.
 XX
 XX 24-JAN-2000; 2000US-00490208.
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Bennett CF, Dean NM, Cowse LM;
 XX
 XX WPI; 2001-465340/50.
 XX
 XX New antisense oligonucleotides for modulating the expression of inducible
 PT nitric oxide synthase in cells or tissues, particularly useful for
 PT treating e.g. immunological, cardiovascular or neurological disorders, or
 PT ischemia.
 XX
 XX Example 15; Page 83; 144pp; English.
 XX
 XX The invention relates to antisense compounds, especially
 CC oligonucleotides, which are targeted to a nucleic acid encoding inducible
 CC nitric oxide synthase and which specifically hybridise to and modulate
 CC expression of inducible nitric oxide synthase. The antisense compounds
 CC have immunomodulator, antidiabetic, cardiovascular, cardiant,
 CC neuroprotective, disorder and vasotropic activity. The antisense
 CC oligonucleotides are useful for inhibiting the expression of inducible
 CC nitric oxide synthase in cells or tissues. In particular, the antisense
 CC oligonucleotides are useful for treating diseases or disorders associated
 CC with inducible nitric oxide synthase, e.g. diabetes, immunological
 CC disorder, cardiovascular disorder, neurological disorder or
 CC ischaemia/reperfusion injury. The antisense oligonucleotides are also
 CC useful for research and diagnostics. The present sequence is that of an

CC antisense 2'-O-methoxyethyl gapmer oligonucleotide with a
 CC phosphorothioate backbone, a central "gap" region of ten nucleotides
 CC flanked by four nucleotide 2'-MOE (2'-methoxyethyl) wings (cytidine
 CC residues in the 2'-MOE wings are 5-methylcytidines) and targeted to human
 CC inducible nitric oxide synthase (NOS) mRNA (AAH47959)
 XX
 SQ Sequence 18 BP; 3 A; 3 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
 |||||
 Db 1 TGTCACTTATCTGGATT 18

RESULT 2

ADQ62106/c
 ID ADQ62106 standard; RNA; 19 BP.
 XX

AC ADQ62106;
 XX

DT 09-SEP-2004 (first entry)
 XX

DE Anti-NOS2A siRNA SEQ ID NO:1808.
 XX

KW ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
 KW RNA interference.
 XX

OS Synthetic.
 XX

PN WO2004045543-A2.
 XX

XX 03-JUN-2004.
 XX

PF 14-NOV-2003; 2003WO-US036787.
 XX

PR 14-NOV-2002; 2002US-0426137P.
 PR 10-SEP-2003; 2003US-0502050P.
 XX

XX (DHAR-) DHARMACON INC.
 XX

PI Anastasia K, Angela R, Devin L, William M, Stephen S;
 XX

DR WPI; 2004-420527/39.
 XX

XX Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases
 PT by selecting a target gene and measuring the functionality of the
 PT nucleotide sequences that are complementary to a stretch of nucleotides
 PT of the target sequence.
 XX

XX Example 12; SEQ ID NO 1808; 199pp; English.
 XX

XX The invention relates to a novel method for selecting siRNA (short
 CC interfering RNA) comprising selecting an siRNA molecule of 19-25
 CC nucleoside bases by selecting a target gene and measuring the
 CC functionality of sequences of 19-25 nucleotides in length that are
 CC substantially complementary to a stretch of nucleotides of the target
 CC sequence, where the functionality is dependent upon non-target specific
 CC criteria. Also claimed are methods for gene-silencing, developing an
 CC siRNA algorithm for selecting siRNA, selecting an siRNA with improved
 CC functionality, selecting hyperfunctional siRNA, an siRNA molecule
 CC effective at silencing Bcl-2, and a kit for gene silencing comprising the
 CC siRNA. The siRNA molecule comprises a sequence substantially similar to a
 CC sequence consisting of GGAGAGUGAGUGAGUGA; GAAGACAUCCAUUUAAG;
 CC GTACGACACCGGAGUA; AGAUGAGUGAGUGACAU; UGAAGACUCUGUCAGUUU;
 CC GAUGGCGCUCUGUUUUG; UCGGCCUCUGUUUUAUU; GAGUAGUGAGUGAGUAC;
 CC GGAGUAGUGAGUGAGUAC; and GAAGACUCUGUCAGUUUUG. The siRNA molecule
 CC comprises a sense strand and an anti-sense strand. The siRNA molecule
 CC comprises a hairpin. The siRNA molecule comprises between 18 and 30 base
 CC pairs. The kit comprises at least two siRNA, comprising a first optimised
 CC siRNA and a second optimised siRNA. The method is useful in selecting

CC siRNA for generating a gene silencing reagent. The present sequence is
CC used in the exemplification of the invention.

XX Sequence 19 BP; 8 A; 3 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 77.8%; Score 14; DB 12; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 2.1e+03; Indels 0; Gaps 0;

XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTCACCTTATCTGG 14

DB 14 TGTCACCTTATCTGG 1

RESULT 3

ID ADRL16179

XX ADRL16179 standard; DNA; 30 BP.

XX AC

XX ADRL16179;

XX 21-OCT-2004 (first entry)

XX Yersinia pestis His-tagged-YscF amplifying PCR primer, HT-YscF Start.

XX Immunogenic; medicament; antibacterial; vaccine; YscF; PCR; primer; ss.

XX Yersinia pestis.

XX US2004151727-A1.

XX 05-AUG-2004.

XX 18-JUL-2003; 2003US-00622220.

XX 31-JAN-2003; 2003US-0444076P.

XX (NILL/) NILLES M L.

XX (MATS/) MATSON J S.

XX Nilles ML, Matson JS;

XX WPI; 2004-570705/55.

XX New immunogenic composition comprises a recombinant YscF protein, useful
XX as a vaccine for providing protection against a pathogen of Yersinia
XX origin or for treating an animal infected with a Yersinia pathogen.

XX Example 1; SEQ ID NO 15; 31pp; English.

XX The present invention provides an immunogenic composition for providing
XX protection to an animal against a pathogen of Yersinia origin. The
XX invention is useful for the manufacture of a medicament for the treatment
XX of a mammal infected with a Yersinia pathogen. The invention acts as an
XX antibacterial and useful for the preparation of a vaccine against a
XX pathogen of Yersinia origin. The present sequence is Yersinia pestis His-
XX tagged (HT)-YscF DNA amplifying PCR primer. This sequence is used in the
XX exemplification of the invention.

XX Sequence 30 BP; 6 A; 7 C; 7 G; 10 T; 0 U; 0 Other;

Query Match 76.7%; Score 13.8; DB 13; Length 30;

XX Best Local Similarity 88.2%; Pred. No. 2.8e+03;

XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACTTATCTGGATT 18

DB 14 GTCACTTATCTGGATT 30

RESULT 4

ADP13976

ID ADP13976 standard; DNA; 25 BP.

XX

AC ADP13976;

XX 26-AUG-2004 (first entry)

XX Renal cell carcinoma differentially expressed gene probe #381.

XX ss; diagnosis; non-blood disease; solid tumor; gene expression;

XX peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;

XX head/neck cancer; differential expression; probe.

XX Homo sapiens.

XX WO2004048933-A2.

XX 10-JUN-2004.

XX 21-NOV-2003; 2003WO-US037481.

XX 21-NOV-2002; 2002US-0427982P.

XX 03-APR-2003; 2003US-0459782P.

XX (AMHP) WYETH.

XX (TWIN/) TWINE N C.

XX (BURC/) BURCZYNSKI M E.

XX (TRBP/) TREPICCHIO W L.

XX (DORN/) DORNER A.

XX (STOV/) STOVER J A.

XX (SLON/) SLONI D K.

XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;

XX PI Sloni DK;

XX WPI; 2004-460799/43.

XX Diagnosing non-blood disease such as solid tumor, involves comparing
XX differential expression profile of specific genes in peripheral blood
XX sample of subject with reference expression profile of specific genes.

XX Disclosure; SEQ ID NO 712; 350pp; English.

XX The invention relate to a method of diagnosing (M1) non-blood disease
XX such as solid tumor by providing peripheral blood sample of human having
XX non-blood disease, and comparing an expression profile of specific genes
XX in the peripheral blood sample to reference expression profile of the
XX genes, where each of the genes is differentially expressed in peripheral
XX blood mononuclear cells (PBMCs) of patients having the disease as
XX compared to PBMCs of normal humans. The method is useful for diagnosing
XX non-blood disease such as solid tumor. The solid tumor is chosen from
XX renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
XX peripheral blood sample comprises enriched PBMCs. The peripheral blood
XX sample is a whole blood sample (claimed). (M1) is useful for identifying
XX genes that are differentially expressed in peripheral blood samples
XX isolated at different stages of progression, development or treatment of
XX RCC and/or other solid tumors. This sequence corresponds to a probe to
XX detect a gene that is differentially expressed and detected by the method
XX of the invention.

XX Sequence 25 BP; 4 A; 6 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 74.4%; Score 13.4; DB 12; Length 25;

XX Best Local Similarity 93.3%; Pred. No. 4.5e+03;

XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CACTTATCTGGATT 18

DB 11 CACTGATCTGGATT 25

RESULT 5

ADP13977

ID ADP13977 standard; DNA; 25 BP.

XX

AC ADP13977;

```

XX DT 26-AUG-2004 (first entry)
XX DE Renal cell carcinoma differentially expressed gene probe #382.
XX DE ss; diagnosis; non-blood disease; solid tumor; gene expression;
XX KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
XX KW head/neck cancer; differential expression; probe.
XX OS Homo sapiens.
XX PN WO2004048933-A2.
XX PD 10-JUN-2004.
XX PF 21-NOV-2003; 2003WO-US037481.
XX PR 21-NOV-2002; 2002US-0427982P.
XX PR 03-APR-2003; 2003US-0459782P.
XX PA (AMHP ) WYETH.
XX PA (TWIN/) TWINE N C.
XX PA (BURC/) BURCZYNSKI M E.
XX PA (TREP/) TREPICCHIO W L.
XX PA (DORN/) DORNER A.
XX PA (STOV/) STOVER J A.
XX PA (SLON/) SLONI D K.
XX PI Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
XX PI Sloni DK;
XX DR WPI; 2004-460799/43.
XX PT Diagnosing non-blood disease such as solid tumor, involves comparing
XX PT differential expression profile of specific genes in peripheral blood
XX PT sample of subject with reference expression profile of specific genes.
XX PS Disclosure; SEQ ID NO 713; 350pp; English.
XX CC The invention relate to a method of diagnosing (M1) non-blood disease
XX CC such as solid tumor by providing peripheral blood sample of human having
XX CC non-blood disease, and comparing an expression profile of specific genes
XX CC in the peripheral blood sample to reference expression profile of the
XX CC genes, where each of the genes is differentially expressed in peripheral
XX CC blood mononuclear cells (PBMCs) of patients having the disease as
XX CC compared to PBMCs of normal humans. The method is useful for diagnosing
XX CC non-blood disease such as solid tumor. The solid tumor is chosen from
XX CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
XX CC sample is a whole blood sample (claimed). (M1) is useful for identifying
XX CC genes that are differentially expressed in peripheral blood samples
XX CC isolated at different stages of progression, development or treatment of
XX CC RCC and/or other solid tumors. This sequence corresponds to a probe to
XX CC detect a gene that is differentially expressed and detected by the method
XX CC of the invention.
XX SQ Sequence 25 BP; 8 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

  Query Match 74.4%; Score 13.4; DB 12; Length 25;
  Best Local Similarity 93.3%; Pred. No. 4.5e+03;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CACTATATCTGATTT 18
   |||||
Db 3 CACTGATCTGATTT 17

RESULT 6
ADL01630
ID ADL01630 standard; DNA; 41 BP.
XX AC ADL01630;
XX
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DT 06-MAY-2004 (first entry)
XX Escherichia coli ydbB PCR primer #3.
XX DE protein co-ordinate data; protein co-ordinate data; ComA; crystal; ydbB;
XX KW PCR; primer; ss.
XX OS Escherichia coli.
XX PN WO2003050239-A2.
XX PD 19-JUN-2003.
XX PF 08-NOV-2002; 2002WO-US036087.
XX PR 09-NOV-2001; 2001US-0337683P.
XX PA (STRU-) STRUCTURAL GENOMIX INC.
XX PI Louie GV, Gajiwala KS, Buchanan SG;
XX DR WPI; 2003-532899/50.
XX PT Producing a computer-readable database comprising three-dimensional
XX PT molecular structural coordinates comprising obtaining three-dimensional
XX PT structural coordinates defining the protein or a binding pocket of the
XX PT protein.
XX PS Example 1; Page 65; 586pp; English.
XX CC The present invention relates to E. coli ComA protein (ADL01638) and its
XX CC protein co-ordinate data. The ComA crystalline protein is a heavy-atom
XX CC derivative crystal. The invention is useful for producing a computer-
XX CC readable database for solving the crystal and solution structures of
XX CC related and unrelated proteins, for screening, identifying and/or
XX CC designing protein analogs and modified proteins or compounds that bind
XX CC and/or modulate a biological activity of ComA or ydbB (ADL01633),
XX CC including inhibitors or activators of ComA or ydbB activity. PCR primers
XX CC from E. coli genomic DNA. The PCR product was then ligated with T4 DNA
XX CC ligase into pSB3. The vector pSB3 is a modified version of pET26b wherein
XX CC the sequence of ADL01632 has been inserted into the NdeI site. The
XX CC resulting sequence of the gene after being ligated into the vector, from
XX CC the Shine-Balgarno sequence through the stop site and the "original"
XX CC BamHI site is given in ADL01629.
XX SQ Sequence 41 BP; 13 A; 9 C; 5 G; 14 T; 0 U; 0 Other;

  Query Match 74.4%; Score 13.4; DB 10; Length 41;
  Best Local Similarity 93.3%; Pred. No. 4.7e+03;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTCACCTTATCTGGA 15
   |||||
Db 13 TGTCCTTATCTGGA 27

RESULT 7
ABN39325
ID ABN39325 standard; DNA; 60 BP.
XX AC ABN39325;
XX DT 15-JUL-2002 (first entry)
XX DE Human spliced transcript detection oligonucleotide SEQ ID NO:12073.
XX KW Human; mouse; rat; splice transcript; detection; RNA transcript;
XX KW splice variant; transcriptome; oligonucleotide library; ss.
XX OS Homo sapiens.
XX PN WO200210449-A2.
```



```

XX PS Example 3; Page 11; 22pp; German.
XX CC This invention describes a novel method for the specific detection and
CC identification of retroviral nucleic acid (or retroviruses) comprising
CC isolation of DNA and/or RNA, subjecting this to reverse transcription-
CC polymerase chain reaction (RT-PCR) with one of two specified primer pairs
CC (or both pairs), purifying the amplicons and analyzing them by reverse
CC dot blot hybridization (RDBH) using immobilized, synthetic
CC oligonucleotide probes. The method is used to detect retroviruses (or
CC their nucleic acid) in cell cultures (or supernatants); body samples or
CC other biological materials. It produces an expression pattern of all
CC retroviruses in a single experiment, particularly for large scale surveys
CC to determine any correlations between diseases and activity of selected
CC retroviruses. If such a correlation is found, the method will allow early
CC diagnosis, or assessment of risk. An efficient, reliable and rapid method
CC for detecting all presently known endogenous and exogenous retroviruses
CC of human or animal origin with very low detection limit. The
CC amplification primers are universal and inclusion of a clamp and
CC restriction enzyme recognition site in them (i) improves primer/matrix
CC binding kinetics and allows amplification of Kase templates even if
CC there is not an exact match and (ii) facilitates subsequent cloning.
CC Using probes that do not overlap with primers overcomes the problem of
CC amplicons reacting, to some extent, with all probes in the array
XX CC
SQ Sequence 45 BP; 11 A; 5 C; 10 G; 19 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 4; Length 45;
Best Local Similarity 83.3%; Pred. No. 6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
Db 3 TATCAGTTATCTGGCTT 20

RESULT 10
ABSS5303
ID ABS55303 standard; DNA; 48 BP.
XX AC ABS55303;
XX DT 12-DEC-2002 (first entry)
XX DE PLAC promoter 5' PCR primer.
XX KW Plasmid; transposon; selectable marker; transposase; promoter;
XX environmentally sensitive; bacterial; origin of replication; viability;
XX bacterial cell; Gram-negative; large-scale screening; gene multiplicity;
XX footprinting plasmid; PCR; primer; ss; PLAC.
XX OS Synthetic.
XX PN US2002119573-A1.
XX PD 29-AUG-2002.
XX PF 28-FEB-2001; 2001US-00796088.
XX PR 28-FEB-2001; 2001US-00796088.
XX PA (SHAW/) SHAW K J.
XX PA (KENN/) KENNEY T.
XX PA (SHIM/) SHIMER G H.
XX PI Shaw KJ, Kenney T, Shimer GH;
XX DR WPI; 2002-740187/80.
XX CC Novel plasmid for determining importance of gene in viability of
XX organism, has transposon having marker gene, gene encoding transposase
XX linked to promoter, and environmentally sensitive bacterial origin of
XX replication.

XX PS Example 1; Page 4; 19pp; English.
XX CC The present invention relates to a new plasmid comprising a transposon
XX carrying a selectable marker gene, a gene encoding a transposase that
XX catalyzes insertion of the transposon into genomic DNA in vivo, where the
XX gene is operably linked to a regulatable promoter, and an environmentally
XX sensitive bacterial origin of replication. The invention is useful for
XX determining if a bacterial gene of interest is important for viability of
XX bacterial cell (Gram-negative) from which it is derived. The invention is
XX also useful for large-scale screening of the multiplicity of genes. The
XX invention allows rapid and efficient determination of the role in cell
XX viability of a large number of genes. The present nucleic acid sequence
XX represents a PCR primer that was used in the invention for construction
XX of footprinting plasmids
SQ Sequence 48 BP; 13 A; 11 C; 6 G; 18 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 6; Length 48;
Best Local Similarity 83.3%; Pred. No. 6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
Db 16 TGTCACTTATCTGGATT 33

RESULT 11
ABSS5302/c
ID ABS55302 standard; DNA; 48 BP.
XX AC ABS55302;
XX DT 12-DEC-2002 (first entry)
XX DE Chloramphenicol (cat) gene 3' PCR primer.
XX KW Plasmid; transposon; selectable marker; transposase; promoter;
XX environmentally sensitive; bacterial; origin of replication; viability;
XX bacterial cell; Gram-negative; large-scale screening; gene multiplicity;
XX footprinting plasmid; PCR; primer; ss; chloramphenicol; cat.
XX OS Unidentified.
XX PN US2002119573-A1.
XX PD 29-AUG-2002.
XX PF 28-FEB-2001; 2001US-00796088.
XX PR 28-FEB-2001; 2001US-00796088.
XX PA (SHAW/) SHAW K J.
XX PA (KENN/) KENNEY T.
XX PA (SHIM/) SHIMER G H.
XX PI Shaw KJ, Kenney T, Shimer GH;
XX DR WPI; 2002-740187/80.
XX CC Novel plasmid for determining importance of gene in viability of
XX organism, has transposon having marker gene, gene encoding transposase
XX linked to promoter, and environmentally sensitive bacterial origin of
XX replication.

XX PS Example 1; Page 4; 19pp; English.
XX CC The present invention relates to a new plasmid comprising a transposon
XX carrying a selectable marker gene, a gene encoding a transposase that
XX catalyzes insertion of the transposon into genomic DNA in vivo, where the
XX gene is operably linked to a regulatable promoter, and an environmentally
XX sensitive bacterial origin of replication. The invention is useful for
XX determining if a bacterial gene of interest is important for viability of

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CC bacterial cell (Gram-negative) from which it is derived. The invention is
 CC also useful for large-scale screening of the multiplicity of genes. The
 CC invention allows rapid and efficient determination of the role in cell
 CC viability of a large number of genes. The present nucleic acid sequence
 CC represents a PCR primer that was used in the invention for construction
 CC of footprinting plasmids

XX Sequence 48 BP; 18 A; 6 C; 11 G; 13 T; 0 U; 0 Other;
 SQ Query Match 73.3%; Score 13.2; DB 6; Length 48;
 Best Local Similarity 83.3%; Pred. NO. 6e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
 |||||
 DB 33 TGTCACTTAACCTGGATT 16

RESULT 12

ABN52886

ID ABN52886 standard; DNA; 65 BP.

AC ABN52886;

DT 15-JUL-2002 (first entry)

DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:25634.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;

KW splice variant; transcriptome; oligonucleotide library; ss.

XX Mus musculus.

PN WO200210449-A2.

XX 07-FEB-2002.

PF 20-JUL-2001; 2001WO-IB001903.

XX 28-JUL-2000; 2000US-0221607P.

PR 02-MAY-2001; 2001US-0287724P.

XX (COMP-) COMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX WPI; 2002-257393/30.

XX New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a
 PT genome, useful for detecting tissue-, pathology-, and developmental-
 PT specific genes.

PS Example 1; SEQ ID NO 25634; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
 CC)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises several
 CC oligonucleotides, each capable of hybridising selectively to a set of
 CC messenger RNAs transcribed from a given transcription unit of the genome,
 CC which encodes one or more messenger RNA splice variants. The
 CC oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterising the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a particular
 CC biological or pathological state, and so allowing the detection of tissue
 CC - and pathology-specific genes such as those genes only expressed in
 CC specific tissue under a specific pathological condition; to detect
 CC developmental specific genes; and to detect RNA transcripts and splice
 CC variants of a transcriptome of a patient suffering from a particular

CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
 CC rats, humans and mice, which are used in the exemplification of the
 CC present invention. N.B. The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at fip.wipo.int/pub/published_pct_sequences

XX Sequence 65 BP; 14 A; 14 C; 19 G; 18 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 6; Length 65;

Best Local Similarity 83.3%; Pred. NO. 6.2e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
 |||||
 DB 32 TGTCACTTATCTGGATAT 49

RESULT 13

ADP80938/C

ID ADP80938 standard; cDNA; 75 BP.

XX AC ADP80938;

XX 09-SEP-2004 (first entry)

DE Mouse DnaJ homologue subfamily A member 2 nucleotide SEQ ID NO:163.

XX c-fos; c-fos interacting protein; fos interacting protein chromosome X;

KW Fip-cx; screening; Fc-fos interacting protein inhibitor; mouse;

KW DnaJ homologue subfamily A member 2; gene; ss.

XX Mus musculus.

XX Key Location/Qualifiers

FT 1..75

FT /*tag= a

FT /product= "DnaJ homologue subfamily A member 2"

XX WO2004053121-A1.

XX 24-JUN-2004.

XX 19-NOV-2003; 2003WO-JP014749.

XX 11-DEC-2002; 2002JP-00360046.

XX (UYKE-) UNIV KEIO.

XX Miyamoto E, Ishizaka M, Yanagawa H;

XX WPI; 2004-517250/49.

XX P-PSDB; ADP80874.

XX New proteins that interact with fos, e.g., fos interacting protein
 PT chromosome X (Fip-cx).

PS Claim 107; SEQ ID NO 163; 192pp; Japanese.

XX The present invention describes a protein (I) that interacts with c-fos
 CC (e.g., fos interacting protein chromosome X (Fip-cx), Fip-cx.1, fos
 CC interacting protein chromosome ex.2, or fos interacting protein
 CC chromosome 4). Also described: (1) a nucleic acid (II) that encodes (I);
 CC an inhibitor (III) that inhibits the interaction of (I) encoded by
 CC (II) with c-fos protein; (3) an inhibitor (IV) that inhibits interaction
 CC of a protein with c-fos protein; and (4) detecting (M1) the interaction
 CC of a protein as mentioned in (3) with c-fos protein, by contacting the
 CC protein with c-fos, to form a complex. (I) is useful for detecting its
 CC interaction with c-fos, to form a complex. (M1) is useful for screening
 CC the protein that interacts with c-fos which involves performing the
 CC detection process and selecting the protein that interacts with c-fos.
 CC (M1) is useful for screening a protein that interacts with c-fos which
 CC involves performing (M1) and selecting the detected protein. (I) is
 CC useful for screening inhibitors that interact with c-fos. The present

CC sequence encodes a mouse DnaJ homologue subfamily A member 2 amino acid
CC sequence, which can interact with c-fos in the exemplification of the
CC present invention.

XX
SQ Sequence 75 BP; 25 A; 13 C; 27 G; 10 T; 0 U; 0 Other;
Query Match 73.3%; Score 13.2; DB 12; Length 75;
Best Local Similarity 83.3%; Pred. No. 6.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
| | | | | | | | | |
Db 23 TCTCGCTTCTCTGGATT 6

RESULT 14
ADU73604
ID ADU73604 standard; DNA; 20 BP.
XX
AC ADU73604;
XX
DT 10-FEB-2005 (first entry)
XX
DE Probe N-STX1-F2 for amplified shiga-like toxin stx1 gene detection.
XX
KW Analyte detection; Nucleic acid detection; chromatography;
KW shiga-like toxin I; probe; ss.
XX
OS Escherichia coli.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= 5' Amine"

XX
XX WO2004099438-A1.
XX
XX 18-NOV-2004.
XX
XX 30-APR-2004; 2004WO-BE000061.
XX
XX 07-MAY-2003; 2003US-0468805P.
XX
XX (CORI-) CORIS BIOCONCEPT SPRL.
XX
XX Renuart I, Mertens P, Leclipteux T;
XX
XX WPI; 2004-821682/81.
XX
XX New sheet-like chromatographic device comprising an application region, a
XX detection region possibly with a control region and optionally an
XX adsorbent region, useful in detecting or quantifying an analyte in a
XX biological sample.
XX
XX Example 2; SEQ ID NO 1; 36pp; English.

XX
CC The invention relates to methods and devices for detecting analytes in a
CC biological sample, preferably a clean liquid sample. Sheet-like
CC oligochromatographic devices are provided, in particular dipsticks, flow-
CC through and lateral flow devices, having an application region
CC (optionally with conjugation pad), a detection region (possibly with
CC control portion, e.g. control lines) and optionally an absorbent region.
CC The detection region comprises at least one capture reagent specifically
CC recognizing a hapten or peptide conjugated with or coupled to an analyte-
CC specific oligonucleotide. The application region comprises at least one
CC specific labeled conjugate (with direct or indirect label) preferably an
CC oligonucleotide (DNA, RNA, PNA, LNA) that hybridizes specifically with
CC the analyte and generally designated as a probe. The device allows the
CC presence of a polynucleotide to be specifically detected directly or
CC after molecular amplification steps. The device is easy to handle and
CC allows rapid but accurate detection and/or diagnosis. The present
CC sequence is that of oligonucleotide probe N-STX1-F2 for the Escherichia

CC coli strain O157:H7 shiga-like toxin I stx1 gene. The probe was used in
CC an example from the invention in which an oligochromatographic dipstick
CC was designed for the specific detection of amplified stx1 and stx2 genes.

XX
SQ Sequence 20 BP; 4 A; 3 C; 3 G; 10 T; 0 U; 0 Other;
Query Match 72.2%; Score 13; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTTATCTGGATT 18
| | | | | | | | | |
Db 4 CTTATCTGGATT 16

RESULT 15
ADR70635
ID ADR70635 standard; DNA; 50 BP.
XX
AC ADR70635;
XX
DT 21-OCT-2004 (first entry)
XX
DE Exemplary set-unique oligonucleotide #4 for Escherichia coli Shiga gene.
XX
KW unique genomic sequence; similarity search engine; genomic database;
KW BLAST search engine; GenBank; ss; Shiga gene.
XX
OS Escherichia coli.
XX
XX WO2004065565-A2.
XX
XX 05-AUG-2004.
XX
XX 23-JAN-2004; 2004WO-US001701.
XX
XX 23-JAN-2003; 2003US-0441745P.
XX
XX 23-JAN-2003; 2003US-0441806P.
XX
XX (SCIT-) SCI APPL INT CORP.
XX
XX Eley DG, Vockley JG;
XX
XX WPI; 2004-562161/54.
XX
XX Identifying genomic and oligonucleotide sequences unique to a set of
XX organisms, useful for gathering sequences on organisms present in a
XX sample, comprises searching selected genomic database using the query and
XX the similarity search engine.
XX
XX Disclosure; Page 20; 34pp; English.

XX
CC The specification describes a method for identifying genomic sequences
XX and oligonucleotide sequences unique to a set of organisms. The method
XX comprises obtaining genomic data characteristic of the set, formatting
XX the genomic data into at least one query-length sequence, each query-
XX length sequence being of a format compatible with a similarity search
XX engine, searching a selected genomic database using the query and the
XX similarity search engine, and parsing the results of the search for those
XX sequences showing uniqueness to the set. The similarity search engine is
XX a BLAST search engine. The selected database is GenBank. The method is
XX useful for identifying genomic sequences and oligonucleotide sequences
XX unique to a set of organisms. The method is also useful for gathering
XX sequences on one or more sets of organisms present in a sample. ADR70632-
XX ADR70641 represent exemplary set-unique oligonucleotides for Escherichia
XX coli Shiga gene, identified using the method of the invention.

XX
SQ Sequence 50 BP; 11 A; 10 C; 10 G; 19 T; 0 U; 0 Other;
Query Match 72.2%; Score 13; DB 13; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PR 26-JUL-1999; 99KR-00031172.
PA (SAMY-) SAMYANG GENEX CORP.
XX
DR WPI; 2001-285602/30.
PT Novel protein involved in encapsulation, used as an immunological
PT activity enhancer.
XX
PS Example 4; Page 6; 23pp; Japanese.
XX
CC The present probe is provided in a specification relating a mealworm
CC protein that participates in encapsulation, which is a cellular defensive
CC reaction. The invention provides an encapsulation polypeptide comprising
CC residues 1-754 or 18-754 of a 754 amino acid sequence, or 1-579 or 16-579
CC residues of a 579 amino acid sequence, both fully defined in the specification, or
CC a mutant having a replacement, deletion or insertion of an amino acid in
CC at least one residue of the sequence. The protein can be used as an
CC immunological activity enhancer
XX
SQ Sequence 23 BP; 9 A; 3 C; 2 G; 2 T; 0 U; 7 Other;
Query Match 71.1%; Score 12.8; DB 4; Length 23;
Best Local Similarity 61.1%; Pred. No. 9.2e+03;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
OY 1 TGTCACCTATCTGGATT 18
Db 19 TTTCTTATATGTAAT 2
RESULT 21
AAD26335
ID AAD26335 standard; DNA; 24 BP.
XX
AC AAD26335;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human beta-tubulin gene exon 1 sequencing SE1 reverse PCR primer.
XX
KW Human; beta-tubulin; GTP-binding site; prognosis; lung cancer;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200190413-A2.
XX
PD 29-NOV-2001.
XX
PF 17-MAY-2001; 2001WO-US016004.
XX
PR 19-MAY-2000; 2000US-00574788.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Rosell R, Monzo M;
XX
WPI; 2002-097668/13.
XX
PT Prognosticating efficacy of anticancer agents in a patient suffering from
PT cancer involves analyzing sample from patient for presence of mutation in
PT GTP-binding site or carboxy-terminal region of exon 4 of tubulin gene.
XX
PS Example 7; Page 22; 26pp; English.
XX
CC The invention relates to a method for prognosticating efficacy of
CC anticancer agent in a patient suffering from cancer. The method involves
CC analysing a biological sample from a patient for the presence of mutation
CC in the GTP-binding site or carboxy-terminal region of exon 4 of mutant
CC tubulin genes. The method is useful for prognosticating the efficacy of
CC anticancer agents (an anti-tubulin agent) in patients suffering from lung
CC cancer. The present sequence is a PCR primer used for sequencing human

CC beta-tubulin gene exon 1
XX
SQ Sequence 24 BP; 5 A; 4 C; 2 G; 13 T; 0 U; 0 Other;
Query Match 71.1%; Score 12.8; DB 6; Length 24;
Best Local Similarity 87.5%; Pred. No. 9.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3 TCACCTTATCTGGATT 18
Db 7 TAACCTACCTGGATT 22
RESULT 22
AAS13868/c
ID AAS13868 standard; DNA; 27 BP.
XX
AC AAS13868;
XX
DT 18-DEC-2001 (first entry)
XX
DE Tn5-based transposon PCR primer Tn7L.PCR.
XX
KW Transposon Tn5; sequencing primer; transposon-disrupted gene;
KW Gene function; ss.
XX
OS Synthetic.
XX
PN WO200171040-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009003.
XX
PR 23-MAR-2000; 2000US-0191561P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Sharpe PL, Cheng Q, Nagatajan V;
XX
WPI; 2001-611517/70.
XX
PT Identifying essential genes responsible for specific phenotypes in
PT microorganisms by inserting a transposon-disrupted gene homolog into the
PT microorganism genome is useful to determine gene function.
XX
PS Example 6; Page 28; 51pp; English.
XX
CC The invention relates to a method of identifying an essential gene
CC responsible for a specific phenotype in a recombination proficient
CC microorganism. The method comprises inserting a transposon-disrupted gene
CC homologue into the microorganism genome and selecting for transformants
CC having a changed phenotype. The method is used to elucidate the function
CC of known gene sequences and can be used on microorganisms which are not
CC naturally transformable. The present sequence represents Tn5-based
CC transposon sequencing primer Tn7L.PCR, used in the method of the
XX invention
XX
SQ Sequence 27 BP; 10 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 71.1%; Score 12.8; DB 4; Length 27;
Best Local Similarity 87.5%; Pred. No. 9.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 TGTCACCTATCTGGATT 16
Db 18 TTTCACTTATCTGGTT 3
RESULT 23
ABZ48041/c
ID ABZ48041 standard; DNA; 41 BP.
XX

[illegible]

CC polymorphism data, particularly that relating to single nucleotide
 CC polymorphisms (SNPs), may be used in studying the relationship between
 CC DNA sequence variations and human diseases, conditions, and responses to
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes
 CC that cause or exacerbate certain diseases. SNPs are particularly useful
 CC in the above respects as they are stable in populations, occur
 CC frequently, and have lower mutation rates than other genome variations
 CC such as repeating sequences. The detection and analysis of polymorphisms
 CC in genes encoding drug metabolising enzymes allows the customisation of
 CC drug therapies based upon the genetic profile of individual patients.
 CC This would not only take the guesswork out of selecting the drug with the
 CC greatest therapeutic effect for a particular patient, but would also
 CC reduce the likelihood of adverse reactions, thereby increasing safety.
 CC Methods of the invention are also useful in the drug discovery and
 CC approval processes. For example, individuals could be selected for
 CC clinical trials only if their genetic profiles indicate that they are
 CC capable of responding to a particular drug or drug class, and previously
 CC failed drug candidates could be revived if they were matched with more
 CC appropriate patient populations. The methods, data and compositions of
 CC the invention may therefore lead to an increase in the range of
 CC possible drug targets and decreases in the number of adverse drug
 CC reactions, failed drug trials, the time taken for a drug to be approved,
 CC the length of time patients are on medication and the number of different
 CC medications a patient needs to take before finding an effective therapy

XX
 SQ Sequence 41 BP; 16 A; 10 C; 8 G; 7 T; 0 U; 0 Other;
 Query Match 71.1%; Score 12.8; DB 6; Length 41;
 Best Local Similarity 87.5%; Pred. No. 9.6e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCACCTTATCTGGATT 18
 Db 41 TTACTTATCAGGATT 26

RESULT 25

AAZ68526/c
 ID AAZ68526 standard; DNA; 47 BP.

AC AAZ68526;

XX 10-SEP-2001 (first entry)

DE Human map-related biallelic marker SEQ ID NO:2874.

XX Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation; diagnosis;
 KW single nucleotide polymorphism; SNP; ds.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH variation replace(24,C)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"

XX WO954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB0000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX

PT Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome.

PS Claim 3; Page 843; 2745pp; English.

XX
 CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention

XX
 SQ Sequence 47 BP; 15 A; 7 C; 7 G; 18 T; 0 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 3; Length 47;
 Best Local Similarity 87.5%; Pred. No. 9.8e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGTCACCTTATCTGGAT 16

Db 22 TATCATTATCTGAAT 7

Search completed: March 3, 2006, 08:00:39
 Job time : 123.534 secs

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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:29:32 ; Search time 23.6441 Seconds
(without alignments)
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Title: US-10-655-801-22

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1395746

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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4: /cgn2_6/prodata/1/ina/6B COMB.seq:
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9: /cgn2_6/prodata/1/ina/6backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	13.4	74.4	25	3	US-09-396-196G-102305
C 2	13.2	73.3	25	3	US-09-396-196G-61721
C 3	13.2	73.3	25	3	US-09-396-196G-111634
C 4	12.8	71.1	19	3	US-09-696-791-2758
C 5	12.8	71.1	19	3	US-09-696-791-2759
C 6	12.8	71.1	27	3	US-09-808-658-7
C 7	12.8	71.1	47	3	US-09-422-978-2874
C 8	12.8	71.1	50	3	US-10-131-827-3958
C 9	12.8	71.1	51	3	US-09-693-146-15
C 10	12.8	71.1	54	3	US-09-693-146-17
C 11	12.4	68.9	15	3	US-09-142-913-26
C 12	12.4	68.9	15	9	5182195-46
C 13	12.4	68.9	25	3	US-09-396-196G-93855
C 14	12.4	68.9	42	2	US-08-790-963-17
C 15	12.4	68.9	42	3	US-09-371-774-17
C 16	12.4	68.9	42	3	US-09-875-082-17
C 17	12.4	68.9	47	3	US-09-422-978-1643
C 18	12.4	68.9	47	3	US-09-422-978-1659
C 19	12.4	68.9	63	3	US-09-513-999C-15454
C 20	12.2	67.8	21	3	US-09-215-221-30
C 21	12.2	67.8	25	3	US-09-396-196G-117798
C 22	12.2	67.8	25	3	US-09-396-196G-117799
C 23	12.2	67.8	30	3	US-09-292-071-6
C 24	12.2	67.8	30	3	US-09-292-071-11

Sequence 6, Appli	30	3	US-09-292-069A-6	67.8	12.2	C 25
Sequence 11, Appli	30	3	US-09-292-069A-11	67.8	12.2	C 26
Sequence 6, Appli	30	3	US-09-418-721-6	67.8	12.2	C 27
Sequence 11, Appli	30	3	US-09-418-721-11	67.8	12.2	C 28
Sequence 6, Appli	30	3	US-09-767-013-6	67.8	12.2	C 29
Sequence 11, Appli	30	3	US-09-767-013-11	67.8	12.2	C 30
Sequence 6, Appli	30	3	US-09-292-072-6	67.8	12.2	C 31
Sequence 11, Appli	30	3	US-09-292-072-11	67.8	12.2	C 32
Sequence 120, App	30	3	US-09-170-496D-120	67.8	12.2	C 33
Sequence 236, App	30	3	US-09-170-496D-236	67.8	12.2	C 34
Sequence 6, Appli	30	3	US-10-176-255-6	67.8	12.2	C 35
Sequence 11, Appli	30	3	US-10-176-255-11	67.8	12.2	C 36
Sequence 20, Appli	31	3	US-09-445-375A-20	67.8	12.2	C 37
Sequence 246, App	37	3	US-09-826-509-246	67.8	12.2	C 38
Sequence 543, App	50	2	US-08-171-389-543	67.8	12.2	C 39
Sequence 543, App	50	2	US-08-123-936-543	67.8	12.2	C 40
Sequence 543, App	50	2	US-08-475-228A-543	67.8	12.2	C 41
Sequence 543, App	50	2	US-08-482-080A-543	67.8	12.2	C 42
Sequence 543, App	50	3	US-08-354-947-543	67.8	12.2	C 43
Sequence 543, App	50	3	US-09-993-346-543	67.8	12.2	C 44
Sequence 74, Appli	50	3	US-10-131-827-74	67.8	12.2	C 45
Sequence 543, App	50	6	PCT-US93-12388-543	67.8	12.2	C 46
Sequence 2066, Ap	53	3	US-08-956-171B-2066	67.8	12.2	C 47
Sequence 101308,	53	3	US-08-781-986A-2066	67.8	12.2	C 48
Sequence 101319,	25	3	US-09-396-196G-101308	66.7	12	C 49
Sequence 101320,	25	3	US-09-396-196G-101319	66.7	12	C 50
Sequence 101321,	25	3	US-09-396-196G-101320	66.7	12	C 51
Sequence 42, Appli	20	2	US-08-474-542A-42	65.6	11.8	C 52
Sequence 42, Appli	20	2	US-08-457-648-42	65.6	11.8	C 53
Sequence 1870, Ap	21	3	US-09-657-472-1870	65.6	11.8	C 54
Sequence 19519, A	25	3	US-09-396-196G-19519	65.6	11.8	C 55
Sequence 19520, A	25	3	US-09-396-196G-19520	65.6	11.8	C 56
Sequence 121239,	25	3	US-09-396-196G-121239	65.6	11.8	C 57
Sequence 39, Appli	32	3	US-08-222-616-39	65.6	11.8	C 58
Sequence 39, Appli	32	3	US-08-446-648-39	65.6	11.8	C 59
Sequence 39, Appli	32	6	PCT-US95-04228-39	65.6	11.8	C 60
Sequence 56, Appli	30	3	US-08-468-352-56	65.6	11.8	C 61
Sequence 1965, Ap	30	3	US-10-131-827-1965	65.6	11.8	C 62
Sequence 31, Appli	57	2	US-08-089-974B-31	65.6	11.8	C 63
Sequence 58, Appli	18	3	US-10-014-012-58	64.4	11.6	C 64
Sequence 190, App	22	3	US-08-983-605-190	64.4	11.6	C 65
Sequence 24, Appli	24	2	US-08-632-575B-24	64.4	11.6	C 66
Sequence 24, Appli	24	3	US-09-199-542B-24	64.4	11.6	C 67
Sequence 25786, A	25	3	US-09-396-196G-25786	64.4	11.6	C 68
Sequence 43129, A	25	3	US-09-396-196G-43129	64.4	11.6	C 69
Sequence 56053, A	25	3	US-09-396-196G-56053	64.4	11.6	C 70
Sequence 59217, A	25	3	US-09-396-196G-59217	64.4	11.6	C 71
Sequence 64715, A	25	3	US-09-396-196G-64715	64.4	11.6	C 72
Sequence 67237, A	25	3	US-09-396-196G-67237	64.4	11.6	C 73
Sequence 78819, A	25	3	US-09-396-196G-78819	64.4	11.6	C 74
Sequence 121367,	25	3	US-09-396-196G-121367	64.4	11.6	C 75
Sequence 121368,	25	3	US-09-396-196G-121368	64.4	11.6	C 76
Sequence 123611,	28	3	US-08-975-982-13	64.4	11.6	C 77
Sequence 13, Appli	29	2	US-08-859-998-1359	64.4	11.6	C 78
Sequence 1359, Ap	29	3	US-09-225-928-1359	64.4	11.6	C 79
Sequence 1359, Ap	29	3	US-09-225-928-1359	64.4	11.6	C 80
Sequence 1359, Ap	29	3	US-09-225-928-1359	64.4	11.6	C 81
Sequence 74, Appli	32	3	US-09-199-542B-74	64.4	11.6	C 82
Sequence 6, Appli	39	3	US-10-211-948-6	64.4	11.6	C 83
Sequence 481, App	47	3	US-09-422-978-481	64.4	11.6	C 84
Sequence 3, Appli	49	2	US-08-392-771-3	64.4	11.6	C 85
Sequence 17, Appli	50	2	US-08-860-882A-17	64.4	11.6	C 86
Sequence 21, Appli	50	3	US-09-423-439-21	64.4	11.6	C 87
Sequence 13, Appli	50	3	US-09-011-769A-13	64.4	11.6	C 88
Sequence 1583, Ap	50	3	US-10-131-827-1583	64.4	11.6	C 89
Sequence 44, Appli	61	3	US-09-171-945-44	64.4	11.6	C 90
Sequence 45, Appli	61	3	US-09-171-945-45	64.4	11.6	C 91
Sequence 44, Appli	61	3	US-09-910-059-44	64.4	11.6	C 92
Sequence 45, Appli	61	3	US-09-910-059-45	64.4	11.6	C 93

OTHER INFORMATION: Cyclin G1 ribozyme binding site
US-09-696-791-2759

Query Match 71.1%; Score 12.8; DB 3; Length 47;
Best Local Similarity 87.5%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels

Qy 1 TGTCATTATCTGGAT 16
|||
Db 22 TATCACTTATCTGAAT 7

RESULT 8

RESULT 8
US-10-131-827-3958
; Sequence 3958, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:

APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc

```

: TITLE OF INVENTION: METHODS AND COMPOSITIONS
:
: TITLE OF INVENTION: CHRONIC INFLAMMATORY
:
: FILE REFERENCE: 506612000120
:
: CURRENT APPLICATION NUMBER: US/10/131,827
:
: CURRENT FILING DATE: 2002-09-06
:

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; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22

; PRIORITY APPLICATION NUMBER: US 60/296,764
; PRIORITY FILING DATE: 2001-06-08

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; PRIOR FILING DATE: 2001 00 00
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1

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; SOFTWARE: F
; SEQ ID NO 39
; LENGTH: 50

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; LENGTH: 50
; TYPE: DNA
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118-10-131-937-3858 ; ORGANISM: HOMO

Query Match 71.1%; Score 12.8; DB 3; Length 50;
Best Local Similarity 87.5%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels

Qy 2 GTCACTTATCTGGATT 17
||| ||| ||| ||| |||
Db 20 GTCTCTTGTCTGGATT 35

RESUMEN 9

RESULT 9
US-09-693-146-15/c
; Sequence 15, Application US/09693146
; Patent No. 6413758
; GENERAL INFORMATION.

; GENERAL INFORMATION:
; APPLICANT: Xu, Shuang-yong
; APPLICANT: Zhu Zhenwu

; APPLICANT: ZHU, Zhenyu
; APPLICANT: Xiao, Jian-ping
; TITLE OF INVENTION: Method

1. TITLE OF INVENTION: Method for Cloning And

; TITLE OF INVENTION: ENDOHUCLEASE IN E. COLI
 ; FILE REFERENCE: NEB-183
 ; CURRENT APPLICATION NUMBER: US/00/593 145

; CURRENT APPLICATION NUMBER: US/09/693,146
 ; CURRENT FILING DATE: 2000-10-20
 NUMBER OF SEQ ID NOS: 10

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; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 15
; LENGTH: 51

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; TYPE: DNA
; ORGANISM: Bacillus pumilus

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US-09-693-146-15

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Query Match      71.1%; Score 12.8; DB 3; Length 51;
Best Local Similarity 87.5%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCACTTATCTGATTT 18
Db 35 TCACTTATATGCATTT 20

RESULT 10
US-09-693-146-17/c
; Sequence 17, Application US/09693146
; Patent No. 6413758
; GENERAL INFORMATION:
; APPLICANT: Xu, Shuang-yong
; APPLICANT: Zhu, Zhenyu
; APPLICANT: Xiao, Jian-ping
; TITLE OF INVENTION: Method For Cloning And Expression Of BpmI Restriction
; FILE OF INVENTION: Endonuclease In E. coli
; FILE REFERENCE: NEB-183
; CURRENT APPLICATION NUMBER: US/09/693,146
; CURRENT FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Bacillus pumilus
US-09-693-146-17

Query Match      71.1%; Score 12.8; DB 3; Length 54;
Best Local Similarity 87.5%; Pred. No. 2.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCACTTATCTGATTT 18
Db 38 TCACTTATATGCATTT 23

RESULT 11
US-09-142-913-26
; Sequence 26, Application US/09142913A
; Patent No. 6573073
; GENERAL INFORMATION:
; APPLICANT: HARRIS, ANN
; TITLE OF INVENTION: CFTR GENE REGULATOR
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/142,913A
; FILING DATE: 18-Sep-1998
; CLASSIFICATION: <Unknown>
; 20-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB97/00787
; FILING DATE: <Unknown>
; APPLICATION NUMBER: GB 9605808.6
; FILING DATE: 20-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1283-37

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-142-913-26

Query Match      68.9%; Score 12.4; DB 3; Length 15;
Best Local Similarity 92.9%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGTCACTTATCTGG 14
Db 1 TGTCACTTATCTGG 14

RESULT 12
5182195-46
; Patent No. 5182195
; APPLICANT: NAKAHAMA, KAZUO;KAISHO, YOSHIHIKO;YOSHIMURA, KOJI
; TITLE OF INVENTION: METHOD FOR INCREASING USING PROTEASE
; DEFICIENT YEASTS
; NUMBER OF SEQUENCES: 71
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/269,140
; FILING DATE: 09-NOV-1988
; SEQ ID NO:46:
; LENGTH: 15
5182195-46

Query Match      68.9%; Score 12.4; DB 9; Length 15;
Best Local Similarity 92.9%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGTCACTTATCTGG 14
Db 1 TGTCACTTATCTGG 14

RESULT 13
US-09-396-196G-93855
; Sequence 93855, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93855
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-93855

Query Match      68.9%; Score 12.4; DB 3; Length 25;
Best Local Similarity 92.9%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTCACTTATCTGGA 15
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Db 1 GTGCACTTATCTGG 14

RESULT 14

US-08-790-963-17/c
; Sequence 17, Application US/08790963
; Patent No. 5837464
; GENERAL INFORMATION:
; APPLICANT: Daniel J. Capon
; APPLICANT: Christos John Petropoulos
; TITLE OF INVENTION: Compositions And Methods For
; TITLE OF INVENTION: Determining Anti-viral Drug Susceptibility And
; TITLE OF INVENTION: Resistance
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,963
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50130-B/JPW/AKC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-790-963-17

Query Match 68.9%; Score 12.4; DB 2; Length 42;
Best Local Similarity 92.9%; Pred. No. 3.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGG 14
Db 17 TGGCACTTATCTGG 4

RESULT 15

US-09-371-774-17/c
; Sequence 17, Application US/09371774
; Patent No. 6242187
; GENERAL INFORMATION:
; APPLICANT: Daniel J. Capon
; APPLICANT: Christos John Petropoulos
; TITLE OF INVENTION: Compositions And Methods For
; TITLE OF INVENTION: Determining Anti-viral Drug Susceptibility And
; TITLE OF INVENTION: Resistance
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States

ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/371,774
; FILING DATE: 10-Aug-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50130-F/JPW/CMR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-371-774-17

Query Match 68.9%; Score 12.4; DB 3; Length 42;
Best Local Similarity 92.9%; Pred. No. 3.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGG 14
Db 17 TGGCACTTATCTGG 4

RESULT 16

US-09-875-082-17/c
; Sequence 17, Application US/09875082
; Patent No. 6942969
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J
; APPLICANT: Petropoulos, Christos J
; TITLE OF INVENTION: Compositions and Methods For Determining Anti-Viral Drug Susceptibility
; TITLE OF INVENTION: and Resistance and Anti-Viral Drug Screening
; FILE REFERENCE: 2793/50130-G
; CURRENT APPLICATION NUMBER: US/09/875,082
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 17
; LENGTH: 42
; TYPE: DNA
; ORGANISM: HUMAN
US-09-875-082-17

Query Match 68.9%; Score 12.4; DB 3; Length 42;
Best Local Similarity 92.9%; Pred. No. 3.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGG 14
Db 17 TGGCACTTATCTGG 4

RESULT 17

US-09-422-978-1643
; Sequence 1643, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya

; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1643
; LENGTH: 47

; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-5364-95 : polymorphic base C or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 47
; OTHER INFORMATION: n=a, g, c or t
US-09-422-978-1643

Query Match 68.9%; Score 12.4; DB 3; Length 47;
Best Local Similarity 81.2%; Pred. No. 3.4e+03;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCACCTATCTGGATT 18
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Db 17 TCACCTATCTGGATT 32

RESULT 18

US-09-422-978-1659/c

; Sequence 1659, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1659
; LENGTH: 47

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: allele

; LOCATION: 24

; OTHER INFORMATION: 99-5438-70 : polymorphic base C or T
US-09-422-978-1659

Query Match 68.9%; Score 12.4; DB 3; Length 47;
Best Local Similarity 81.2%; Pred. No. 3.4e+03;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCACCTATCTGGATT 18
|||||:|||||
Db 30 TCACCTATCTGGATT 15

RESULT 19

US-09-513-999C-15454/c

; Sequence 15454, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 15454
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-15454

Query Match 68.9%; Score 12.4; DB 3; Length 63;
Best Local Similarity 92.9%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ACTTATCTGGATT 18
|||||:|||||
Db 49 ACATATCTGGATT 36

RESULT 20

US-09-215-221-30/c

; Sequence 30, Application US/09215221
; Patent No. 6265562
; GENERAL INFORMATION:
; APPLICANT: EILERS, MARTIN
; APPLICANT: BUERGIN, ANDREA
; APPLICANT: SEDLACEK, HANS-HARALD
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCTS WHOSE ACTIVITY IS AFFECTED BY
; TITLE OF INVENTION: INHIBITORS OF CYCLIN-DEPENDANT KINASES AND USES THEREOF
; FILE REFERENCE: 026083/0192
; CURRENT APPLICATION NUMBER: US/09/215,221
; CURRENT FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 197 56 975.7
; PRIOR FILING DATE: 1997-12-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-215-221-30

Query Match 67.8%; Score 12.2; DB 3; Length 21;
Best Local Similarity 82.4%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GTCACCTATCTGGATT 18
|||||:|||||
Db 18 GACGCTTTCTGGATT 2

RESULT 21

US-09-396-196G-117798

; Sequence 117798, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart

;; APPLICANT: Affymetrix, Inc.
;; TITLE OF INVENTION: Methods of Genetic Analysis
;; FILE REFERENCE: 3101.1
;; CURRENT APPLICATION NUMBER: US/09/396,196G
;; CURRENT FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: 60/100,678
;; PRIOR FILING DATE: 1998-09-17
;; NUMBER OF SEQ ID NOS: 127806
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 117798
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: mus musculus
US-09-396-196G-117798

Query Match 67.8%; Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 4.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GTCACTTATCTGGATT 18
DB 9 GTCACTTATATGCGCTT 25

RESULT 22
US-09-396-196G-117799
; Sequence 117799, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Wittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117799
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-117799

Query Match 67.8%; Score 12.2; DB 3; Length 25;
Best Local Similarity 82.4%; Pred. No. 4.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GTCACTTATCTGGATT 18
DB 3 GTCACTTATATGCGCTT 19

RESULT 23
US-09-292-071-6/c
; Sequence 6, Application US/09292071
; Patent No. 6107324
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic
; APPLICANT: Chalmers, Derick
; TITLE OF INVENTION: No. 6107324-Endogenous, Constitutively Activated
; TITLE OF INVENTION: Human Serotonin Receptors and Small Molecule Modulators Thereof
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arena Pharmaceuticals, Inc.
; STREET: 6166 Nancy Ridge Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/292,071
;; FILING DATE: April 14, 1999
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mark J. Rosen
;; REGISTRATION NUMBER: 39,822
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 564-6525
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 30 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-09-292-071-6

Query Match 67.8%; Score 12.2; DB 3; Length 30;
Best Local Similarity 82.4%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 17
DB 25 TTTCACCTATCTGGAAT 9

RESULT 24
US-09-292-071-11/c
; Sequence 11, Application US/09292071
; Patent No. 6107324
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic
; APPLICANT: Chalmers, Derick
; TITLE OF INVENTION: No. 6107324-Endogenous, Constitutively Activated
; TITLE OF INVENTION: Human Serotonin Receptors and Small Molecule Modulators Thereof
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arena Pharmaceuticals, Inc.
; STREET: 6166 Nancy Ridge Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/292,071
; FILING DATE: April 14, 1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Rosen
; REGISTRATION NUMBER: 39,822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 564-6525
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-292-071-11

Query Match 67.8%; Score 12.2; DB 3; Length 30;
 Best Local Similarity 82.4%; Pred. No. 4.2e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGTCACTTATCTGGATT 17
 | | | | | | | | | |
 Db 25 TTTCACCTATCTGGAA 9

RESULT 25
 US-09-292-069A-6/c
 ; Sequence 6, Application US/09292069A
 ; Patent No. 6140509
 ; GENERAL INFORMATION:
 ; APPLICANT: Behan, Dominic P
 ; APPLICANT: Chalmers, Derek T
 ; APPLICANT: Foster, Richard J
 ; APPLICANT: Glen, Robert C
 ; APPLICANT: Lawless, Michael S
 ; APPLICANT: Liaw, Chen W
 ; APPLICANT: Liu, Qian
 ; APPLICANT: Russo, Joseph F
 ; APPLICANT: Smith, Julian R
 ; APPLICANT: Thomsen, William J
 ; TITLE OF INVENTION: No. 6140509-Endogenous, Constitutively Activated Human
 ; TITLE OF INVENTION: Serotonin Receptors And Small Molecule Modulators
 ; TITLE OF INVENTION: Thereof
 ; FILE REFERENCE: AREN0033
 ; CURRENT APPLICATION NUMBER: US/09/292.069A
 ; CURRENT FILING DATE: 1999-04-14
 ; PRIOR APPLICATION NUMBER: 60/090,783
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/112,909
 ; PRIOR FILING DATE: 1998-12-18
 ; PRIOR APPLICATION NUMBER: 60/123,000
 ; PRIOR FILING DATE: 1999-03-05
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 30
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: No. 6140509el
 ; OTHER INFORMATION: Sequence
 ; US-09-292-069A-6

Query Match 67.8%; Score 12.2; DB 3; Length 30;
 Best Local Similarity 82.4%; Pred. No. 4.2e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGTCACTTATCTGGATT 17
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 Db 25 TTTCACCTATCTGGAA 9

Search completed: March 3, 2006, 07:34:55
 Job time : 24.6441 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:34:36 ; Search time 221.11 Seconds
 (without alignments)
 673.188 Million cell updates/sec

Title: US-10-655-801-22

Perfect score: 18

Sequence: 1 tgtcattctgtgattt 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11282798

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA_Main:

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- 2: /cgn2_6/prodata1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/prodata1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/prodata1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/prodata1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/prodata1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/prodata1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/prodata1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/prodata1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/prodata1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	9	US-10-182-049-22	Sequence 22, Appl
2	15.4	85.6	25	10	US-11-036-317-457256	Sequence 457256,
3	14.8	82.2	25	8	US-10-719-900-965964	Sequence 965964,
4	14.4	80.0	25	8	US-10-719-900-661094	Sequence 661094,
5	14	77.8	25	8	US-10-719-900-41145	Sequence 41145, A
6	14	77.8	25	10	US-11-036-317-127763	Sequence 127763,
7	14	77.8	25	10	US-11-036-317-746021	Sequence 746021,
8	13.8	76.7	25	7	US-10-719-956-489627	Sequence 489627,
9	13.8	76.7	25	7	US-10-719-956-489628	Sequence 489628,
10	13.8	76.7	25	7	US-10-719-956-493504	Sequence 493504,
11	13.8	76.7	25	8	US-10-719-900-138687	Sequence 138687,
12	13.8	76.7	25	8	US-10-719-900-398525	Sequence 398525,
13	13.8	76.7	25	8	US-10-719-900-426089	Sequence 426089,
14	13.8	76.7	25	8	US-10-719-900-443222	Sequence 443222,
15	13.8	76.7	25	8	US-10-719-900-443223	Sequence 443223,
16	13.8	76.7	25	8	US-10-719-900-723091	Sequence 723091,
17	13.8	76.7	25	8	US-10-719-900-790694	Sequence 790694,
18	13.8	76.7	25	8	US-10-719-900-901150	Sequence 901150,
19	13.8	76.7	25	10	US-11-036-317-21790	Sequence 21790, A
20	13.8	76.7	30	7	US-10-622-220-15	Sequence 15, Appl
21	13.4	74.4	25	7	US-10-717-597-712	Sequence 712, App
22	13.4	74.4	25	7	US-10-717-597-713	Sequence 713, App
23	13.4	74.4	25	7	US-10-719-956-132748	Sequence 132748,

24	13.4	74.4	25	8	US-10-719-900-69367	Sequence 69367, A
25	13.4	74.4	25	8	US-10-719-900-359264	Sequence 359264,
26	13.4	74.4	25	8	US-10-719-900-383984	Sequence 383984,
27	13.4	74.4	25	8	US-10-719-900-557493	Sequence 557493,
28	13.4	74.4	25	8	US-10-719-900-870061	Sequence 870061,
29	13.4	74.4	25	8	US-10-719-900-966596	Sequence 966596,
30	13.4	74.4	25	9	US-10-809-189-102305	Sequence 102305,
31	13.4	74.4	25	10	US-11-036-317-462752	Sequence 462752,
32	13.4	74.4	41	6	US-10-291-851-8	Sequence 8, Appl
33	13.4	74.4	60	3	US-09-908-975-12073	Sequence 12073, A
34	13.2	73.3	21	6	US-10-108-260A-4958	Sequence 4958, AP
35	13.2	73.3	25	7	US-10-719-956-281385	Sequence 281385,
36	13.2	73.3	25	7	US-10-719-956-395340	Sequence 395340,
37	13.2	73.3	25	7	US-10-719-956-415591	Sequence 415591,
38	13.2	73.3	25	7	US-10-719-956-535367	Sequence 535367,
39	13.2	73.3	25	7	US-10-719-956-581172	Sequence 581172,
40	13.2	73.3	25	7	US-10-719-956-668305	Sequence 668305,
41	13.2	73.3	25	8	US-10-719-900-281343	Sequence 281343,
42	13.2	73.3	25	8	US-10-719-900-413325	Sequence 413325,
43	13.2	73.3	25	8	US-10-719-900-543959	Sequence 543959,
44	13.2	73.3	25	8	US-10-719-900-562112	Sequence 562112,
45	13.2	73.3	25	8	US-10-719-900-835724	Sequence 835724,
46	13.2	73.3	25	8	US-10-719-900-909419	Sequence 909419,
47	13.2	73.3	25	8	US-10-719-900-933964	Sequence 933964,
48	13.2	73.3	25	8	US-10-719-900-960944	Sequence 960944,
49	13.2	73.3	25	9	US-10-809-189-965963	Sequence 965963,
50	13.2	73.3	25	9	US-10-809-189-61721	Sequence 61721, A
51	13.2	73.3	25	9	US-10-809-189-111634	Sequence 111634,
52	13.2	73.3	25	10	US-11-036-317-27577	Sequence 27577, A
53	13.2	73.3	25	10	US-11-036-317-174886	Sequence 174886,
54	13.2	73.3	25	10	US-11-036-317-205667	Sequence 205667,
55	13.2	73.3	25	10	US-11-036-317-213977	Sequence 213977,
56	13.2	73.3	25	10	US-11-036-317-232234	Sequence 232234,
57	13.2	73.3	25	10	US-11-036-317-349126	Sequence 349126,
58	13.2	73.3	25	10	US-11-036-317-387997	Sequence 387997,
59	13.2	73.3	25	10	US-11-036-317-469248	Sequence 469248,
60	13.2	73.3	25	10	US-11-036-317-862786	Sequence 862786,
61	13.2	73.3	25	10	US-11-036-317-879623	Sequence 879623,
62	13.2	73.3	25	10	US-11-036-317-884780	Sequence 884780,
63	13.2	73.3	25	10	US-11-036-317-940977	Sequence 940977,
64	13.2	73.3	25	10	US-11-036-317-962992	Sequence 962992,
65	13.2	73.3	25	10	US-11-060-756-155037	Sequence 155037,
66	13.2	73.3	25	10	US-11-060-756-292291	Sequence 292291,
67	13.2	73.3	48	3	US-09-796-088-2	Sequence 2, Appl
68	13.2	73.3	65	3	US-09-796-088-3	Sequence 3, Appl
69	13.2	73.3	65	3	US-09-908-975-25634	Sequence 25634, A
70	13	72.2	25	7	US-10-719-956-182012	Sequence 182012,
71	13	72.2	25	7	US-10-719-956-495658	Sequence 495658,
72	13	72.2	25	8	US-10-719-900-237378	Sequence 237378,
73	13	72.2	25	8	US-10-719-900-392875	Sequence 392875,
74	13	72.2	25	8	US-10-719-900-800945	Sequence 800945,
75	13	72.2	25	10	US-11-036-317-469059	Sequence 469059,
76	13	72.2	25	10	US-11-036-317-559012	Sequence 559012,
77	12.8	71.1	25	7	US-10-681-773-71482	Sequence 71482, A
78	12.8	71.1	25	7	US-10-719-956-39982	Sequence 39982, A
79	12.8	71.1	25	7	US-10-719-956-155360	Sequence 155360,
80	12.8	71.1	25	7	US-10-719-956-270449	Sequence 270449,
81	12.8	71.1	25	7	US-10-719-956-491268	Sequence 491268,
82	12.8	71.1	25	7	US-10-719-956-966332	Sequence 966332,
83	12.8	71.1	25	8	US-10-719-900-64101	Sequence 64101, A
84	12.8	71.1	25	8	US-10-719-900-79886	Sequence 79886, A
85	12.8	71.1	25	8	US-10-719-900-179842	Sequence 179842,
86	12.8	71.1	25	8	US-10-719-900-438745	Sequence 438745,
87	12.8	71.1	25	8	US-10-719-900-482304	Sequence 482304,
88	12.8	71.1	25	8	US-10-719-900-661095	Sequence 661095,
89	12.8	71.1	25	8	US-10-719-900-901060	Sequence 901060,
90	12.8	71.1	25	8	US-10-719-900-920917	Sequence 920917,
91	12.8	71.1	25	9	US-10-956-157-237735	Sequence 237735,
92	12.8	71.1	25	9	US-10-843-527-46162	Sequence 46162, A
93	12.8	71.1	25	9	US-10-843-527-47134	Sequence 47134, A
94	12.8	71.1	25	9	US-10-843-527-47139	Sequence 47139, A
95	12.8	71.1	25	9	US-10-843-527-118490	Sequence 118490,
96	12.8	71.1	25	9	US-10-843-527-118758	Sequence 118758,

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c 97 12.8 71.1 25 9 US-10-843-527-118953 Sequence 118953,
98 12.8 71.1 25 9 US-10-843-527-119224 Sequence 119224,
c 99 12.8 71.1 25 9 US-10-843-527-119419 Sequence 119419,
100 12.8 71.1 25 9 US-10-843-527-119687 Sequence 119687,

ALIGNMENTS

RESULT 1
US-10-182-049-22
; Sequence 22, Application US/10182049
; Publication No. US20050113322A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowbert
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSION
; FILE REFERENCE: R7SP-0360
; CURRENT APPLICATION NUMBER: US/10/182,049
; CURRENT FILING DATE: 2002-07-27
; PRIOR APPLICATION NUMBER: 09/490,208
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-182-049-22

Query Match 100.0%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCACCTTATCTGGATTT 18
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Db 1 TGTCACCTTATCTGGATTT 18

RESULT 2
US-11-036-317-457256/c
; Sequence 457256, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 457256
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-457256

Query Match 85.6%; Score 15.4; DB 10; Length 25;
Best Local Similarity 94.1%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTGACCTTATCTGGATTT 18
| | | | | | | | | | | | | | | |
Db 19 GTGACCTTATCTGGATTT 3

RESULT 3
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US-10-719-900-965964
; Sequence 965964, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 965964
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-965964

Query Match 82.2%; Score 14.8; DB 8; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGTCACCTTATCTGGATTT 18
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Db 6 TGTCACCTTATCTGGATTT 23

RESULT 4
US-10-719-900-661094/c
; Sequence 661094, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 661094
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-661094

Query Match 80.0%; Score 14.4; DB 8; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TCACCTTATCTGGATTT 18
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Db 18 TCACCTTATCTGGATTT 3

RESULT 5
US-10-719-900-41145
; Sequence 41145, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 41145
; LENGTH: 25
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; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-41145

Query Match      77.8%; Score 14; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TCACCTTATCTGGAT 16
Db 11 TCACCTTATCTGGAT 24

RESULT 6
US-11-036-317-127763
; Sequence 127763, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 127763
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-127763

Query Match      77.8%; Score 14; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTCACCTTATCTGGA 15
Db 5 GTCACCTTATCTGGA 18

RESULT 7
US-11-036-317-746021
; Sequence 746021, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 746021
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-746021

Query Match      77.8%; Score 14; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTCACCTTATCTGGA 15
Db 5 GTCACCTTATCTGGA 18

RESULT 8
US-10-719-956-489627
; Sequence 489627, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 489627
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-489627

Query Match      76.7%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GTCACCTTATCTGGA 18
Db 1 GTCACCTTATCTGGA 17

RESULT 9
US-10-719-956-489628
; Sequence 489628, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 489628
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-489628

Query Match      76.7%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GTCACCTTATCTGGA 18
Db 1 GTCACCTTATCTGGA 17

RESULT 10
US-10-719-956-493504
; Sequence 493504, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 493504
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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-493504

Query Match      76.7%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTCACCTTATCTGGATTT 18
    ||||| ||||| |||||
Db 1 GTCCCGTATCTGGATTT 17

RESULT 11
US-10-719-900-138687/c
; Sequence 138687, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 138687
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-138687

Query Match      76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTCACCTTATCTGGATTT 18
    ||||| ||||| |||||
Db 19 GTCTGTTATCTGGATTT 3

RESULT 12
US-10-719-900-398525
; Sequence 398525, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 398525
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-398525

Query Match      76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGTCACTTATCTGGATT 17
    ||||| ||||| |||||
Db 3 TGTCACTGATCTGGAAT 19

RESULT 13
US-10-719-900-426089/c
; Sequence 426089, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 426089
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-426089

Query Match      76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGTCACTTATCTGGATT 17
    ||||| ||||| |||||
Db 18 TATCACTTATCTGGCTT 2

RESULT 14
US-10-719-900-443222/c
; Sequence 443222, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 443222
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-443222

Query Match      76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTCACCTTATCTGGATTT 18
    ||||| ||||| |||||
Db 20 GTCACCTTGTCTGGTTT 4

RESULT 15
US-10-719-900-443223/c
; Sequence 443223, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 443223
; LENGTH: 25
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; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-443223

Query Match      76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTATCTCGGATT 18
   ||||| ||||| |||||
Db 20 GTCACCTATCTCGGTTT 4

RESULT 16
US-10-719-900-723091
; Sequence 723091, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 723091
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-723091

Query Match      76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTATCTCGGATT 18
   ||||| ||||| |||||
Db 1 GTTACCTATCTCGGATT 17

RESULT 17
US-10-719-900-790694
; Sequence 790694, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 790694
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-790694

Query Match      76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 17
   ||||| ||||| |||||
Db 9 TGTCACTTAACTGGATT 25

RESULT 18
US-10-719-900-901150
; Sequence 901150, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 901150
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-901150

Query Match      76.7%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 17
   ||||| ||||| |||||
Db 1 TGTCACTTATCTGGATT 17

RESULT 19
US-11-036-317-21790
; Sequence 21790, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 21790
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-21790

Query Match      76.7%; Score 13.8; DB 10; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 17
   ||||| ||||| |||||
Db 5 TGTGACTTCTCTGGATT 21

RESULT 20
US-10-622-220-15
; Sequence 15, Application US/10622220
; Publication No. US20040151727A1
; GENERAL INFORMATION:
; APPLICANT: Nilles, Matthew L.
; APPLICANT: Matson, Jyl S.
; TITLE OF INVENTION: YERSINIA SPECIES COMPOSITIONS
; FILE REFERENCE: 3128-60460S
; CURRENT APPLICATION NUMBER: US/10/622,220
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/444,076
; PRIOR FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
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; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer, HT-YscF Start
US-10-622-220-15

Query Match      76.7%; Score 13.8; DB 7; Length 30;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGATT 18
Db 14 GTAACCTCTCTGGATT 30

RESULT 21
US-10-717-597-712
; Sequence 712, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dörner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 712
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-712

Query Match      74.4%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CACTTATCTGGATT 18
Db 11 CACTGATCTGGATT 25

RESULT 22
US-10-717-597-713
; Sequence 713, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dörner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21

; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 713
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-713

Query Match      74.4%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CACTTATCTGGATT 18
Db 3 CACTGATCTGGATT 17

RESULT 23
US-10-719-956-132748
; Sequence 132748, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 132748
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-132748

Query Match      74.4%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGAT 16
Db 8 GTCACCTGTCTGGAT 22

RESULT 24
US-10-719-900-69367
; Sequence 69367, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 69367
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-69367

Query Match      74.4%; Score 13.4; DB 8; Length 25;
Best Local Similarity 93.3%; Pred. No. 7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGAT 16
Db 10 GTCACCTATCTGGAT 24
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RESULT 25

US-10-719-900-359264
 ; Sequence 359264, Application US/10719900
 ; Publication No. US20050026164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002 11 20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 359264
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-719-900-359264

Query Match 74.4%; Score 13.4; DB 8; Length 25;
 Best Local Similarity 93.3%; Pred. No. 7e+03; 1; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGTCACTTATCTGGA 15
 | | | | | | | | | | | | | | | |
 Db 3 TTTCACCTATCTGGA 17

Search completed: March 3, 2006, 08:48:51
 Job time : 223.11 secs

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OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:35:12 ; Search time 97.8559 Seconds
(without alignments)
403.294 Million cell updates/sec

Title: US-10-655-801-22

Perfect score: 18
Sequence: 1 tgtcacttctgtgattt 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Capext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 11869656

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications_NA_New.*

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- 2: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/prodata/1/pubpna/US05_NEW_PUB.seq.*
- 6: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq.*
- 7: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq.*
- 8: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq.*
- 9: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
- 12: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq.*
- 13: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
C 1	15	83.3	19 10	US-11-101-244-338677 Sequence 338677,
C 2	15	83.3	19 10	US-11-101-244-338777 Sequence 338777,
C 3	15	83.3	19 11	US-11-083-784-338677 Sequence 338677,
C 4	15	83.3	19 11	US-11-083-784-338777 Sequence 338777,
C 5	14.8	82.2	19 10	US-11-101-244-1064558 Sequence 1064558,
C 6	14.8	82.2	19 11	US-11-083-784-1064558 Sequence 1064558,
C 7	14.8	82.2	25 12	US-11-121-849-547246 Sequence 547246,
C 8	14.4	80.0	18 8	US-10-310-914A-218367 Sequence 218367,
C 9	14.4	80.0	25 12	US-11-121-849-244518 Sequence 244518,
C 10	14.4	80.0	25 12	US-11-175-859-7311 Sequence 7311, Ap
C 11	14.4	80.0	50 12	US-11-175-859-30578 Sequence 30578, A
C 12	14.4	80.0	50 12	US-11-175-859-30594 Sequence 30594, A
C 13	14.4	80.0	69 8	US-10-310-914A-4848 Sequence 4848, Ap
C 14	14	77.8	19 10	US-11-101-244-1808 Sequence 1808, Ap
C 15	14	77.8	19 10	US-11-101-244-338658 Sequence 338658,
C 16	14	77.8	19 10	US-11-101-244-338758 Sequence 338758,
C 17	14	77.8	19 10	US-11-101-244-1284075 Sequence 1284075,
C 18	14	77.8	19 11	US-11-083-784-1808 Sequence 1808, Ap
C 19	14	77.8	19 11	US-11-083-784-338658 Sequence 338658,
C 20	14	77.8	19 11	US-11-083-784-338758 Sequence 338758,

Sequence 1284075,	19	11	US-11-083-784-1284075	77.8	14	C 21
Sequence 284878,	25	12	US-11-121-849-284878	76.7	22	C 22
Sequence 300225,	25	12	US-11-121-849-300225	76.7	23	C 23
Sequence 645767,	25	12	US-11-121-849-645767	76.7	24	C 24
Sequence 14753, A	50	12	US-11-175-859-14753	76.7	25	C 25
Sequence 77157, A	50	12	US-11-175-859-77157	76.7	26	C 26
Sequence 314899,	19	10	US-11-101-244-314899	74.4	27	C 27
Sequence 726306,	19	10	US-11-101-244-726306	74.4	28	C 28
Sequence 894551,	19	10	US-11-101-244-894551	74.4	29	C 29
Sequence 1304787,	19	10	US-11-101-244-1304787	74.4	30	C 30
Sequence 1587155,	19	10	US-11-101-244-1587155	74.4	31	C 31
Sequence 123048,	19	10	US-11-083-784-123048	74.4	32	C 32
Sequence 591731,	25	12	US-11-121-849-591731	74.4	33	C 33
Sequence 41701, A	50	12	US-11-175-859-41701	74.4	34	C 34
Sequence 43502, A	50	12	US-11-175-859-43502	74.4	35	C 35
Sequence 86772, A	50	12	US-11-175-859-86772	74.4	36	C 36
Sequence 111852,	50	12	US-11-175-859-111852	74.4	37	C 37
Sequence 786862,	19	8	US-10-310-914A-786862	73.3	38	C 38
Sequence 880993,	19	10	US-11-101-244-880993	73.3	39	C 39
Sequence 1385488,	19	10	US-11-101-244-1385488	73.3	40	C 40
Sequence 880993,	19	11	US-11-083-784-880993	73.3	41	C 41
Sequence 1385488,	19	11	US-11-083-784-1385488	73.3	42	C 42
Sequence 984742,	21	8	US-10-310-914A-984742	73.3	43	C 43
Sequence 508577,	22	8	US-10-310-914A-508577	73.3	44	C 44
Sequence 523134,	22	8	US-10-310-914A-523134	73.3	45	C 45
Sequence 508523,	24	8	US-10-310-914A-508523	73.3	46	C 46
Sequence 508578,	24	8	US-10-310-914A-508578	73.3	47	C 47
Sequence 561020,	25	12	US-11-121-849-561020	73.3	48	C 48
Sequence 603782,	25	12	US-11-121-849-603782	73.3	49	C 49
Sequence 43559, A	50	12	US-11-175-859-43559	72.2	50	C 50
Sequence 338688,	19	10	US-11-101-244-338688	72.2	51	C 51
Sequence 338788,	19	10	US-11-101-244-338788	72.2	52	C 52
Sequence 672128,	19	10	US-11-101-244-672128	72.2	53	C 53
Sequence 672128,	19	10	US-11-101-244-672128	72.2	54	C 54
Sequence 1449129,	19	10	US-11-101-244-1449129	72.2	55	C 55
Sequence 1449164,	19	10	US-11-101-244-1449164	72.2	56	C 56
Sequence 338688,	19	11	US-11-083-784-338688	72.2	57	C 57
Sequence 338788,	19	11	US-11-083-784-338788	72.2	58	C 58
Sequence 672128,	19	11	US-11-083-784-672128	72.2	59	C 59
Sequence 672225,	19	11	US-11-083-784-672225	72.2	60	C 60
Sequence 1449129,	19	11	US-11-083-784-1449129	72.2	61	C 61
Sequence 1449164,	19	11	US-11-083-784-1449164	72.2	62	C 62
Sequence 338688,	19	11	US-11-083-784-338688	72.2	63	C 63
Sequence 338788,	19	11	US-11-083-784-338788	72.2	64	C 64
Sequence 672128,	19	11	US-11-083-784-672128	72.2	65	C 65
Sequence 672225,	19	11	US-11-083-784-672225	72.2	66	C 66
Sequence 1449129,	19	11	US-11-083-784-1449129	72.2	67	C 67
Sequence 1449164,	19	11	US-11-083-784-1449164	72.2	68	C 68
Sequence 1449165,	19	11	US-11-083-784-1449165	72.2	69	C 69
Sequence 168002,	25	12	US-11-136-527-168002	72.2	70	C 70
Sequence 168003,	25	12	US-11-136-527-168003	72.2	71	C 71
Sequence 168008,	25	12	US-11-136-527-168008	72.2	72	C 72
Sequence 168010,	25	12	US-11-136-527-168010	72.2	73	C 73
Sequence 168021,	25	12	US-11-136-527-168021	72.2	74	C 74
Sequence 168031,	25	12	US-11-136-527-168031	72.2	75	C 75
Sequence 168031,	25	12	US-11-136-527-168031	72.2	76	C 76
Sequence 246131,	25	12	US-11-136-527-246131	72.2	77	C 77
Sequence 246131,	25	12	US-11-136-527-246131	72.2	78	C 78
Sequence 22404, A	50	12	US-11-175-859-22404	72.2	79	C 79
Sequence 62174, A	50	12	US-11-175-859-62174	72.2	80	C 80
Sequence 97672, A	19	10	US-11-101-244-97672	71.1	81	C 81
Sequence 97690, A	19	10	US-11-101-244-97690	71.1	82	C 82
Sequence 184653,	19	10	US-11-101-244-184653	71.1	83	C 83
Sequence 184653,	19	10	US-11-101-244-184653	71.1	84	C 84
Sequence 186192,	19	10	US-11-101-244-186192	71.1	85	C 85
Sequence 186192,	19	10	US-11-101-244-186192	71.1	86	C 86
Sequence 281506,	19	10	US-11-101-244-281506	71.1	87	C 87
Sequence 287716,	19	10	US-11-101-244-287716	71.1	88	C 88
Sequence 502784,	19	10	US-11-101-244-502784	71.1	89	C 89
Sequence 948857,	19	10	US-11-101-244-948857	71.1	90	C 90
Sequence 987398,	19	10	US-11-101-244-987398	71.1	91	C 91
Sequence 1064515,	19	10	US-11-101-244-1064515	71.1	92	C 92
Sequence 1218412,	19	10	US-11-101-244-1218412	71.1	93	C 93

94 12.8 71.1 19 10 US-11-101-244-1218433, Sequence 1218433,
c 95 12.8 71.1 19 11 US-11-083-784-97672 Sequence 97672, A
c 96 12.8 71.1 19 11 US-11-083-784-97690 Sequence 97690, A
97 12.8 71.1 19 11 US-11-083-784-184653 Sequence 184653, A
98 12.8 71.1 19 11 US-11-083-784-184665 Sequence 184665, A
c 99 12.8 71.1 19 11 US-11-083-784-186192 Sequence 186192, A
c 100 12.8 71.1 19 11 US-11-083-784-186223 Sequence 186223, A

ALIGNMENTS

RESULT 1

US-11-101-244-338677/c
; Sequence 338677, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 338677
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-338677

Query Match 83.3%; Score 15; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACTTATCTGGATT 18
|||||
Db 19 CACTTATCTGGATT 5

RESULT 2

US-11-101-244-338777/c
; Sequence 338777, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 338777
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens

US-11-101-244-338777

Query Match 83.3%; Score 15; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACTTATCTGGATT 18
|||||
Db 19 CACTTATCTGGATT 5

RESULT 3

US-11-083-784-338677/c
; Sequence 338677, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 338677
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-338677

Query Match 83.3%; Score 15; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACTTATCTGGATT 18
|||||
Db 19 CACTTATCTGGATT 5

RESULT 4

US-11-083-784-338777/c
; Sequence 338777, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 338777


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; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-338777

Query Match      83.3%; Score 15; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACTTATCTGGATT 18
    |||||
Db 19 CACTTATCTGGATT 5

RESULT 5
US-11-101-244-1064558
; Sequence 1064558, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1064558
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1064558

Query Match      82.2%; Score 14.8; DB 10; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
    |||||
Db 1 UGUCACAUUCUGGAGUU 18

RESULT 6
US-11-083-784-1064558
; Sequence 1064558, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary

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; SEQ ID NO 1064558
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1064558

Query Match      82.2%; Score 14.8; DB 11; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
    |||||
Db 1 UGUCACAUUCUGGAGUU 18

RESULT 7
US-11-121-849-547246
; Sequence 547246, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673304
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 547246
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-547246

Query Match      82.2%; Score 14.8; DB 12; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
    |||||
Db 3 TGTGACCTATCTGGATT 20

RESULT 8
US-10-310-914A-218367/c
; Sequence 218367, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 218367
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-218367

Query Match      80.0%; Score 14.4; DB 8; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCACCTTATCTGGATT 18
    |||||
Db 18 TCATTATCTGGATT 3

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RESULT 9
US-11-121-849-244518/c
; Sequence 244518, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 244518
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-244518

Query Match      80.0%; Score 14.4; DB 12; Length 25;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY      2 GTCACTTATCTGGATT 17
Db      16 GTCAATTATCTGGATT 1

RESULT 10
US-11-175-859-7311/c
; Sequence 7311, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175.859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7311
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-7311

Query Match      80.0%; Score 14.4; DB 12; Length 50;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 TGTCATTATCTGGATT 18
Db      36 TGTCATTATSTTGATT 19

RESULT 11
US-11-175-859-30578
; Sequence 30578, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175.859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
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; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30578
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-30578

Query Match      80.0%; Score 14.4; DB 12; Length 50;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 TCACCTTATCTGGATT 18
Db      3 TCAATTATCTGGATT 18

RESULT 12
US-11-175-859-30594/c
; Sequence 30594, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175.859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30594
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-30594

Query Match      80.0%; Score 14.4; DB 12; Length 50;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 TCACCTTATCTGGATT 18
Db      17 TCAATTATCTGGATT 2

RESULT 13
US-10-310-914A-4848
; Sequence 4848, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4848
; LENGTH: 69
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-4848

Query Match      80.0%; Score 14.4; DB 8; Length 69;
Best Local Similarity 43.8%; Pred. No. 3.7e+02;
Matches 7; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY      3 TCACCTTATCTGGATT 18
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Db 14 TGCTACTTATCTGG 1

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RESULT 16
US-11-101-244-338758/c
; Sequence 338758, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional sirna
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 338758
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-338758

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Query Match      77.8%; Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e-02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  TGTCACTTATCTGG 14
         |||||
Db      14  TGTCACTTATCTGG 1

```

```

RESULT 17
US-11-101-244-1284075/c
; Sequence 1284075, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 159191
; SOFTWARE: Proprietary
; SEQ ID NO 1284075
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1284075

```

```

Query Match      77.8%; Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. NO. 4.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TGTCACTTATCTGG 14
         |||||
Db       14  TGTCACTTATCTGG 1

```

RESULT 18
US-11-083-784-1808/c
; Sequence 1808, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1808
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1808

Query Match 77.8%; Score 14; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGG 14
DB 14 TGTCACTTATCTGG 1

RESULT 19
US-11-083-784-338658/c
; Sequence 338658, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 338658
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-338658

Query Match 77.8%; Score 14; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGG 14
DB 14 TGTCACTTATCTGG 1

RESULT 20
US-11-083-784-338758/c
; Sequence 338758, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 338758
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-338758

Query Match 77.8%; Score 14; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGG 14
DB 14 TGTCACTTATCTGG 1

RESULT 21
US-11-083-784-1284075/c
; Sequence 1284075, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1284075
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1284075

Query Match 77.8%; Score 14; DB 11; Length 19;

```
Best Local Similarity 100.0%; Pred. No. 4.6e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 1 TGTCACTTATCTGG 14
    |||||
Db 14 TGTCACTTATCTGG 1

RESULT 22
US-11-121-849-284878
; Sequence 284878, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 284878
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-284878

Query Match 76.7%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGATT 18
    |||||
Db 8 GTCAGTTATCTGATT 24

RESULT 23
US-11-121-849-300225/c
; Sequence 300225, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 300225
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-300225

Query Match 76.7%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 17
    |||||
Db 17 TGTCACTTCTCTAGATT 1

RESULT 24
US-11-121-849-645767/c
; Sequence 645767, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
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APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded :
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 645767
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-645767

Query Match 76.7%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGATT 18
    |||||
Db 20 GGCACCTTATCTGGTTT 4

RESULT 25
US-11-175-859-14753/c
; Sequence 14753, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14753
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-14753

Query Match 76.7%; Score 13.8; DB 12; Length 50;
Best Local Similarity 88.2%; Pred. No. 7.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTTATCTGGATT 18
    |||||
Db 18 GTTACTTCTCTGGATT 2

Search completed: March 3, 2006, 07:56:44
Job time : 99.0559 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 3, 2006, 07:25:53 ; Search time 984.737 Seconds
(without alignments)
855.220 Million cell updates/sec

Title: US-10-655-801-22

Perfect score: 18
Sequence: 1 tgcacttcttgcgattt 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 512758

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_hc:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_gsa1:
10: gb_gsa2:
11: gb_gsa3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13.4	74.4	69	10	AG193818 Pan trogl
2	13.4	74.4	80	9	CC593206 CH240 394
3	13.2	73.3	34	10	CZ194924 PST14206-
4	13.2	73.3	52	1	AW694082 NF072C05S
5	13.2	73.3	53	10	AG201984 Pan trogl
6	13.2	73.3	62	9	BH810871 SALK 0513
7	13.2	73.3	65	3	BM886513 sam17f01
8	13.2	73.3	74	8	DN430770 LIB4217-0
9	12.8	71.1	37	8	DR1033143 JHU025B06
10	12.8	71.1	38	10	BX659120 Arabidops
11	12.8	71.1	57	7	CV519718 0089P0033
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13	12.8	71.1	68	11	CR111866 Forward s
14	12.8	71.1	77	9	AZ374283 CR249388
15	12.8	71.1	77	9	BH643554 1008058F0
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17	12.4	68.9	24	9	AZ303688 1M0003M11
18	12.4	68.9	62	3	BP080139 BP080139
19	12.4	68.9	74	1	AV963593 AV963593
20	12.2	67.8	42	11	TA92F10Q AL462451 T. Brucei
21	12.2	67.8	50	1	AI308308 ta90f01.x
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59	11	CR061632	Reverse s
25	6	CD940007	RAA 94 Ge
26	6	CD948191	SAD 45 Ge
27	6	CD948787	SAH 116 G
28	6	CB298000	12B22006
29	6	CN545516	EST 17460
30	9	BZ353869	SALK 1222
31	10	CW990741	BB0131 Sa
32	6	AZ348360	1M0084E11
33	6	CD928058	GR45 1030
34	6	CD957750	SCL 33 Ge
35	11	DQ044542	Pan trogl
36	7	AZ824720	2M0099D01
37	11	DQ044541	Homo sapi
38	10	AL944230	Arabidops
39	10	CG507308	OST57211
40	12	CF845484	PSHB033XC
41	37	AA500031	vi96e11.f
42	10	CZ487542	f04956-3p
43	46	BZ663309	SALK 0269
44	9	BH847074	SALK 0130
45	11	AZ604141	1M0423B23
46	1	AJ929315	AJ929315
47	56	1	AJ935185
48	56	1	AJ935523
49	59	1	AZ509880
50	62	CF292190	14ROOT--0
51	62	CF793802	SALK 0186
52	64	BH220392	1006094C0
53	66	CD391037	Gm CK0466
54	66	AZ360386	1M0103C11
55	67	1	AA878568
56	68	AZ962147	2M0230C21
57	68	9	BH810780
58	68	9	BH846857
59	69	9	AZ615106
60	75	10	AL946811
61	76	1	AI609425
62	76	2	BE857854
63	76	8	DN336290
64	76	9	BH855752
65	77	10	BX292494
66	77	11	CR034215
67	79	1	AA623234
68	79	8	AZ21465
69	79	10	AL940313
70	26	10	CG722225
71	35	9	AZ428773
72	35	9	BH908235
73	36	10	AJ593904
74	37	1	AU258765
75	39	9	BZ381294
76	43	9	BH790170
77	44	7	CV293350
78	45	9	BZ384356
79	46	8	D18692
80	46	3	BM889473
81	49	9	AZ776863
82	51	9	AZ797131
83	51	9	BH810529
84	53	9	BH810530
85	53	9	BZ662063
86	54	11	DE000867
87	55	9	BZ354029
88	55	10	CL301069
89	56	9	CT795632
90	56	11	CR250663
91	58	8	D18271
92	58	9	AZ789582
93	59	9	AZ591500
94	59	10	AJ595268
95	60	6	CB217727

96 11.6 64.4 61 1 AA845045 AA845045 ak58b04.s
 c 97 11.6 64.4 61 6 CD941107 CD941107 RAX 45 Ge
 c 98 11.6 64.4 64 8 DN878559 DN878559 nae2id02
 c 99 11.6 64.4 64 9 AZ922054 AZ922054 HRCotIF07
 100 11.6 64.4 66 9 BH902829 BH902829 SALU_1010

ALIGNMENTS

RESULT 1
 AGI93818
 LOCUS
 DEFINITION Pan troglodytes DNA, clone: RP43-071D13.T7, genomic survey
 sequence.
 ACCESSION AGI93818
 VERSION AGI93818.1 GI:45225994
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM
 Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Pan.

REFERENCE 1
 AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C. J.,
 Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 BAC end sequences of Library RP-43
 TITLE Unpublished
 JOURNAL
 REFERENCE 2 (bases 1 to 69)
 AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C. J.,
 Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 Direct Submission
 TITLE Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
 Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
 (E-mail: redstone@mail.krribb.re.kr, URL: http://phs.grc.krribb.re.kr/,
 Tel: 82-42-866-7181, Fax: 82-42-860-4409)
 Clones are derived from the chimpanzee BAC library RP-43. This BAC
 end was generated during the R&D process and may have higher chance
 of clone tracking errors.
 PRIMERS

Sequencing: T7

LIBRARY
 Vector : pBACe3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI.

FEATURES

source
 1..69
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="RP43-071D13.T7"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 74.4%; Score 13.4; DB 10; Length 69;
 Best Local Similarity 93.3%; Pred. No. 4.9e+04;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CACTTATCTGGATT 18

|||||

8 CACTTATATGGATT 22

RESULT 2

CC593206
 LOCUS
 DEFINITION CH240_394G6.TABAC13P2 CHORI-240 Bos taurus genomic clone
 CH240_394G6, genomic survey sequence.
 ACCESSION CC593206
 VERSION CC593206.1 GI:31952671

KEYWORDS

SOURCE

ORGANISM

GSS.
 Bos taurus (cow)
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.

REFERENCE

AUTHORS

1 (bases 1 to 80)
 Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,
 Tsai, M., Cloutier, A., Lee, D., Girm, N., Olson, T., Mayo, M.,
 Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,
 Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,
 Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W.,
 Dalrymple, B. P. and Tellam, R.

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398

JOURNAL

COMMENT

Unpublished (2003)
 Other_GSSs: CH240_394G6.T7

Contact: Rob Holt

Sequencing

The British Columbia Cancer Agency Genome Science Centre

600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6

Tel: 604-877-6085

Fax: 604-877-6276

Email: rhoit@bcgsc.ca

Clones are derived from the bovine BAC library CHORI-240

(http://www.chori.org/bacpac/bovine240.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/ordering.information.htm). This work

was undertaken as part of the International Bovine BAC Mapping

Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the

British Columbia Genome Sciences Centre, Canada.

Plate: 394 row: G column: 6

Seq primer: SP6

Class: BAC ends.

FEATURES

source

1..80
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 /mol_type="genomic DNA"
 /strain="breed: Hereford"
 /db_xref="taxon:9913"
 /clone="CH240_394G6"
 /sex="Male"
 /cell_type="Blood"
 /clone_lib="CHORI-240"
 /note="Vector: pTABAC1.3; Site 1: MboI; Site 2: MboI;
 Hereford bull LI Domino 99375; CHORI-240 Bovine BAC
 library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 74.4%; Score 13.4; DB 9; Length 80;
 Best Local Similarity 93.3%; Pred. No. 5e+04;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CACTTATCTGGATT 18

|||||

64 CACATATCTGGATT 78

RESULT 3

LOCUS

DEFINITION

CZ194924
 PST14206-NR MICB1 Mus musculus genomic clone PST14206-NR, genomic
 survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CZ194924
 CZ194924.1 GI:58833368
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Mus.
 1 (bases 1 to 34)
 Hicks, G.G.

TITLE JOURNAL COMMENT

www.EScells.ca
Unpublished (2002)
Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, University of Manitoba
QW5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
Email: hickegg@cc.umanitoba.ca
U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
sequence information and target gene cloning can be generated. ES
cell line harboring insertion mutation of target gene is available.
Sequence analysis available from
'http://140.193.242.7/esdb/PSTReport.php?PST=PST14206-NR'
Class: Gene Trap.

FEATURES source

Location/Qualifiers
1. .34
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST14206-NR"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
/notes="Vector: U3NeoSV1"

ORIGIN

Query Match 73.3%; Score 13.2; DB 10; Length 34;
Best Local Similarity 83.3%; Pred. No. 5.8e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
|||||
Db 26 TGTCACTTATCTGGATT 9

RESULT 4 AW694082/c LOCUS

DEFINITION
NF072C05ST1F1037 Developing stem Medicago truncatula cDNA clone
NF072C05ST 5', mRNA sequence.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AW694082 52 bp mRNA linear EST 20-DEC-2000
Medicago truncatula (barrel medic)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE AUTHORS

1 (bases 1 to 52)
He, X.-Z., Shadle, G., Scott, A.D., Harris, A.R., Gonzales, R.A.,
Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and
Dixon, R.A.

TITLE JOURNAL COMMENT

Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula stem library
Unpublished (2000)
On Apr 14, 2000 this sequence version replaced gi:7568819.
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org

Insert Length: 714 Std Error: 0.00 Plate: 072 row: C column: 05 Seq primer: TCACACGGAACAGCTATGAC.

FEATURES source

Location/Qualifiers
1. .52
/organism="Medicago truncatula"

Query Match Best Local Similarity Matches

73.3%; Score 13.2; DB 10; Length 34;
83.3%; Pred. No. 5.8e+04;
15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
|||||
Db 26 TGTCACTTATCTGGATT 9

/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF072C05ST"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/clone_lib="Developing stem"
/note="Vector: Lambda Zap; Contains a mixture of
internodal stem segments"

ORIGIN

Query Match 73.3%; Score 13.2; DB 1; Length 52;
Best Local Similarity 83.3%; Pred. No. 6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
|||||
Db 43 TGTCACTTATCTGGATT 26

RESULT 5 AG201984 LOCUS

DEFINITION
Pan troglodytes DNA, clone: RP43-084N15.TJ, genomic survey
sequence.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AG201984 53 bp DNA linear GSS 06-MAR-2004
AG201984.1 GI:45234159
Pan troglodytes (chimpanzee)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.

REFERENCE AUTHORS

1
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

TITLE JOURNAL REFERENCE AUTHORS

BAC end sequences of Library RP-43
Unpublished
2 (bases 1 to 53)
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

TITLE JOURNAL

Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea
(E-mail: redstone@mail.kribb.re.kr, URL: http://phs.grc.kribb.re.kr/
Tel: 82-42-866-7181, Fax: 82-42-860-4409)

COMMENT

Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.

PRIMERS

Sequencing: TJ

LIBRARY

Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.

FEATURES source

Location/Qualifiers
1. .53
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-084N15.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 73.3%; Score 13.2; DB 10; Length 53;
Best Local Similarity 83.3%; Pred. No. 6.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
|||||
Db 8 TCACACTTATCTGGATT 25

RESULT 6
LOCUS BH810871/c
DEFINITION SALK_051322 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_051322, genomic survey sequence.
ACCESSION BH810871
VERSION BH810871.1 GI:20398689
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 62)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of At2g33540.
CLASS: TDNA tagged.
LOCATION/Qualifiers
FEATURES
source
1. .62
/organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_051322"
/notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
Query Match 73.3%; Score 13.2; DB 9; Length 62;
Best Local Similarity 83.3%; Pred.No. 6.2e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TGTCACCTTATCTGGATT 18
|||||
Db 52 TGTAAATATCTGGTTT 35
RESULT 7
LOCUS BM886513
DEFINITION sam17f01.y1 Gm-c1068 Glycine max cDNA clone SOYBEAN CLONE ID:
ACCESSION Gm-c1068-5233 5', mRNA sequence.
VERSION BM886513
KEYWORDS BM886513.1 GI:19270257
SOURCE EST.
ORGANISM Glycine max (soybean)
REFERENCE 1 (bases 1 to 65)
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
TITLE 1 (bases 1 to 65)
AUTHORS Direct Submission (Staten,N.R.)
TITLE Direct Submission (Staten,N.R.)

AUTHORS
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Corryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, F., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson.wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Putative full length read vector to vector length is 66
Seq primer: -40RP from Gibco.

FEATURES
source
1. .65
/organism="Glycine max"
/mol type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1068-5233"
/issue type="Leaf, drought stressed, 1 month old plants, greenhouse grown"
/lab host="DH10B"
/clone lib="Gm-c1068"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from drought stressed leaf tissue of the cultivar Williams 82. The month old greenhouse grown plants were deprived of water for 3 days prior to harvesting the stressed leaf tissue. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN
Query Match 73.3%; Score 13.2; DB 3; Length 65;
Best Local Similarity 83.3%; Pred.No. 6.2e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TGTCACCTTATCTGGATT 18
|||||
Db 23 TGTCACCTTATCTGTATAT 40
RESULT 8
LOCUS DN430770
DEFINITION LIB4217-011-R1-K1-G5 LIB4217 Canis familiaris cDNA clone
ACCESSION CLN10755221, mRNA sequence.
VERSION DN430770
KEYWORDS DN430770.1 GI:60627015
SOURCE EST.
ORGANISM Canis familiaris (dog)
REFERENCE 1 (bases 1 to 74)
AUTHORS Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
TITLE 1 (bases 1 to 74)
AUTHORS Direct Submission (Staten,N.R.)
TITLE Direct Submission (Staten,N.R.)

JOURNAL Unpublished (2005)
COMMENT Contact: Nick Staten
Tel: 636 247 6855
Email: nicholas.r.staten@fizer.com.

FEATURES
source Location/Qualifiers
1..74
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="beagle"
/db_xref="taxon:9615"
/clone="CLN10755221"
/tissue_type="left atrium"
/lab_host="DH108"
/clone_lib="LIB4217"
/notes="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; mixed"

ORIGIN
Query Match 73.3%; Score 13.2; DB 8; Length 74;
Best Local Similarity 83.3%; Pred. NO. 6.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 18
|||||
Db 38 TTTTACTTATCTGGATT 55

RESULT 9
LOCUS DR103143
DEFINITION JHU025B06L37 Canine cardiovascular system biased cDNA Canis familiaris cDNA, mRNA sequence.
ACCESSION DR103143
VERSION DR103143.1 GI:67562498
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris

REFERENCE
AUTHORS DiSilvestre, D., Yung, C., Gao, Z., Farukhi, Y., Winslow, R.L. and Tomaselli, G.F.
TITLE Canine cardiovascular system biased cDNA sequences
JOURNAL Unpublished (2005)
COMMENT Contact: Gordon F. Tomaselli
Johns Hopkins University
720 Rutland Avenue/Ross 844, Baltimore, MD 21205, USA
Tel: 4109552774
Fax: 4105022096
Email: gtomasel@jhmi.edu.

FEATURES
source Location/Qualifiers
1..37
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Mixed"
/db_xref="taxon:9615"
/sex="Mixed"
/clone_lib="Canine cardiovascular system biased cDNA"
/notes="Organ: Mixed; Vector: PCDNA3.1; Site_1: EcoRI; Site_2: XhoI; Adult tissue from eye, lung, aorta, pulmonary artery and brain; neonatal tissue from liver, spleen, thymus, lung, kidney, aorta and brain; 50% is from cardiac tissues."

ORIGIN
Query Match 71.1%; Score 12.8; DB 8; Length 37;
Best Local Similarity 87.5%; Pred. NO. 9.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCACCTTATCTGGATT 18
|||||
Db 16 TCACCTTATCTGGATT 31

RESULT 10
LOCUS BX659120/c
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-643A04-022303, genomic survey sequence.
ACCESSION BX659120
VERSION BX659120.1 GI:37615508
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060
REFERENCE
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321
REFERENCE
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weisshaar, B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL BioTechniques 35 (6), 1164-1168 (2003)
PUBMED 14692050
REFERENCE
AUTHORS Rosso, M.G., Strizhov, N., Li, Y. and Weisshaar, B.
TITLE Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At2g05420. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
1..38
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-643A04-022303"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match 71.1%; Score 12.8; DB 10; Length 38;
Best Local Similarity 87.5%; Pred. NO. 9.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACTTATCTGGATT 17
|||||
Db 34 GTGACTTATTTGGATT 19

```

RESULT 11
CV519718/c
LOCUS
DEFINITION
0089P00332.x0 D01 Mimulus guttatus library 2 Mimulus guttatus cDNA
CV519718
ACCESSION
CV519718
VERSION
CV519718.1 GI:53846250
KEYWORDS
EST.
SOURCE
Mimulus guttatus (spotted monkey flower)
ORGANISM
Mimulus guttatus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Lamiales; Phrymaceae; Mimulus.
1 (bases 1 to 57)
Willis, J., Vision, T., Dietrich, P.S. and Allen, A.
Mimulus guttatus cDNA sequence
TITLE
Unpublished (2004)
JOURNAL
COMMENT
Contact: Willis J
Department of Biology
Duke University
072-A Biological Sciences Science Drive, Durham, NC 27708, USA
Tel: 919 660 7340
Fax: 919 660 7293
Email: jwillis@duke.edu
Plate: 0089P0033 row: 01 column: D
Seq primer: T7
High quality sequence start: 15
High quality sequence stop: 622.
Location/Qualifiers
FEATURES
source
1..57
/organism="Mimulus guttatus"
/mol_type="mRNA"
/db_xref="taxon:4155"
/clone="0089P00332.x0_D01"
/clone_lib="Mimulus guttatus library 2"
/note="Vector: pGEM-T Easy; a Mimulus guttatus cDNA
library"

ORIGIN
Query Match 71.1%; Score 12.8; DB 7; Length 57;
Best Local Similarity 87.5%; Pred. No. 9.8e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTCACTTATCTGGATT 17
|| |||||
Db 52 GTTCTTATCTGGATT 37

RESULT 12
CV519718/c
LOCUS
DEFINITION
Reverse strand read from insert in 5'HPRT insertion targeting and
chromosome engineering clone MHPN311c07, genomic survey sequence.
CV519718
ACCESSION
CV519718.1 GI:50028241
VERSION
CV519718.1 GI:50028241
KEYWORDS
GSS; genome survey sequence; MICR.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 57)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J. and Bradley, A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICR
Location/Qualifiers
FEATURES
source
1..57
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN311c07"
/clone_lib="MHPN"

ORIGIN
Query Match 71.1%; Score 12.8; DB 11; Length 68;
Best Local Similarity 87.5%; Pred. No. 1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGTCACCTTATCTGGAT 16
|| |||||
Db 29 TGCCACATATCTGGAT 44

RESULT 13
CV519718/c
LOCUS
DEFINITION
Reverse strand read from insert in 3'HPRT insertion targeting and
chromosome engineering clone MHPN332a03, genomic survey sequence.
CV519718
ACCESSION
CV519718.1 GI:49859281
VERSION
CV519718.1 GI:49859281
KEYWORDS
GSS; genome survey sequence; MICR.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 68)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J. and Bradley, A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICR
Location/Qualifiers
FEATURES
source
1..68
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN332a03"
/clone_lib="MHPN"

ORIGIN
Query Match 71.1%; Score 12.8; DB 11; Length 68;
Best Local Similarity 87.5%; Pred. No. 1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGTCACCTTATCTGGAT 16
|| |||||
Db 29 TGCCACATATCTGGAT 44

RESULT 14
CV519718/c
LOCUS
DEFINITION
Reverse strand read from insert in 5'HPRT insertion targeting and
chromosome engineering clone MHPN311c07, genomic survey sequence.
CV519718
ACCESSION
CV519718.1 GI:50028241
VERSION
CV519718.1 GI:50028241
KEYWORDS
GSS; genome survey sequence; MICR.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 57)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J. and Bradley, A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICR
Location/Qualifiers
FEATURES
source
1..57
/organism="Mus musculus"
/mol_type="genomic DNA"

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/db_xref="taxon:10090"
/clone="MHPN311c07"
/clone_lib="MHPN"

ORIGIN
Query Match 71.1%; Score 12.8; DB 11; Length 57;
Best Local Similarity 87.5%; Pred. No. 9.8e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCACTTATCTGGATT 18
|| |||||
Db 9 TCACTTATCTGGATT 24

RESULT 13
CV519718/c
LOCUS
DEFINITION
Forward strand read from insert in 3'HPRT insertion targeting and
chromosome engineering clone MHPN332a03, genomic survey sequence.
CV519718
ACCESSION
CV519718.1 GI:49859281
VERSION
CV519718.1 GI:49859281
KEYWORDS
GSS; genome survey sequence; MICR.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 68)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J. and Bradley, A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICR
Location/Qualifiers
FEATURES
source
1..68
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN332a03"
/clone_lib="MHPN"

ORIGIN
Query Match 71.1%; Score 12.8; DB 11; Length 68;
Best Local Similarity 87.5%; Pred. No. 1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGTCACCTTATCTGGAT 16
|| |||||
Db 29 TGCCACATATCTGGAT 44

RESULT 14
CV519718/c
LOCUS
DEFINITION
Reverse strand read from insert in 5'HPRT insertion targeting and
chromosome engineering clone MHPN311c07, genomic survey sequence.
CV519718
ACCESSION
CV519718.1 GI:50028241
VERSION
CV519718.1 GI:50028241
KEYWORDS
GSS; genome survey sequence; MICR.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 77)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

```

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0126 row: 1 column: 19
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 77.
Location/Qualifiers

FEATURES

source

1. .77
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIW0126119"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGCIW library"
/notes="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 71.1%; Score 12.8; DB 9; Length 77;
Best Local Similarity 87.5%; Pred. No. 1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCACCTATCTCGATT 18
|||||
Db 57 TCACATATCTGGCTTT 72

RESULT 15

BH643554/c

LOCUS

DEFINITION 77 bp DNA linear GSS 14-FEB-2002
1008058F09.1EL.Y1 1008 - RescueMu Grid I Zea mays genomic, genomic survey sequence.

ACCESSION

BH643554

VERSION

BH643554.1

KEYWORDS

GSS.

SOURCE

Zea mays

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 77)

Walbot, V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

CONTACT: Walbot V

Department of Biological Sciences

Stanford University

FEATURES

source

1. .77
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/Al88/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1008 - RescueMu Grid I"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site www.zmdb.iastate.edu and follow the links for 'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 71.1%; Score 12.8; DB 9; Length 77;
Best Local Similarity 87.5%; Pred. No. 1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCACCTATCTCGATT 17
|||||
Db 24 GTCACCTTAGCTGAATT 9

RESULT 16

AL796390/c

LOCUS

DEFINITION 78 bp mRNA linear EST 13-NOV-2003
AL796390 XGC-neurula Xenopus tropicalis cDNA clone TNeul28114 5', mRNA sequence.

ACCESSION

AL796390

VERSION

AL796390.2

KEYWORDS

EST.

SOURCE

Xenopus tropicalis (western clawed frog)

ORGANISM

Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 78)

Croning, M.D.R., Ahurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.

Sanger Xenopus tropicalis EST project 2001 (11_2003)

Unpublished (2003)

On Jun 25, 2002 this sequence version replaced gi:21582094.

Contact: Taylor R

Sanger Institute

Hinxtion, Cambridgeshire, CB10 1SA, UK

Email: trop@sanger.ac.uk

This sequence is from a Xenopus Gene Collection (XGC) library

constructed by Aaron M. Zorn.

cDNA was oligo dt primed from 5ug of poly A+ RNA from neurula.

EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the

5' end and NotI at the 3' end.

Vector: pCS107; Site 1: EcoRI; Site 2: NotI

Host: Escherichia coli DH10B

Sanger Xenopus tropicalis EST project 2001

TROPICALIS SEQUENCE ID: TNeul28114.picSP6

Sequencing primer: SP6.

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1008058 row: 11

Class: transposon-tagged.

Location/Qualifiers

```

FEATURES
  source
    Location/Qualifiers
      1..78
        /organism="Xenopus tropicalis"
        /mol_type="mRNA"
        /db_xref="taxon:8364"
        /clone="TNeu128114"
        /dev_stage="neurula"
        /lab_host="Escherichia coli DH10B"
        /clone_lib="XGC-neurula"
        /notes="vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
        was oligo dt primed from Sug of poly A+ RNA from neurula.
        EcoRI-NotI cut cDNA was then ligated into pCS107 with
        EcoRI at the 5' end and NotI at the 3' end."

ORIGIN
  Query Match      71.1%; Score 12.8; DB 1; Length 78;
  Best Local Similarity 87.5%; Pred. No. 1e+05;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCACCTTATCTGGATT 18
   ||||| |||||
Db 44 TCACCTTCTCAGGATT 29

RESULT 17
AZ303688 24 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION
  IM0003M11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0003M11 F, genomic survey sequence.
ACCESSION
  AZ303688
VERSION
  AZ303688.1 GI:10339066
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
  ORGANISM
    Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognath; Muroidae; Muridae; Murinae; Mus.
  1 (bases 1 to 24)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  JOURNAL
  COMMENT
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: dunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0003 row: M column: 11
    Seq primer: CGTTGTAAACGACGCCAGT
    Class: plasmid ends
    High quality sequence stop: 24.
    Location/Qualifiers
      1..24
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC1M0003M11"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /notes="vector: pMD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a

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0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
  Query Match      68.9%; Score 12.4; DB 9; Length 24;
  Best Local Similarity 92.9%; Pred. No. 1.4e+05;
  Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACTTATCTCGATT 18
   ||||| |||||
Db 5 ACTTATCTCGATAT 18

RESULT 18
BP080139 62 bp mRNA linear EST 27-AUG-2004
LOCUS
DEFINITION
  BP080139 Lotus japonicus roots Lotus corniculatus var. japonicus
  cDNA clone MR054b08_f 3', mRNA sequence.
ACCESSION
  BP080139
VERSION
  BP080139.1 GI:45636800
KEYWORDS
  EST.
SOURCE
  Lotus corniculatus var. japonicus (Lotus japonicus)
  ORGANISM
    Eukaryote; Viridiplantae; Streptophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Lotaeae;
    Lotus.
  1 (bases 1 to 62)
  Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  Characteristics of the Lotus japonicus gene repertoire deduced from
  large-scale expressed sequence tag (EST) analysis
  Plant Mol. Biol. 54 (3), 405-414 (2004)
  15284495
  Contact: Erika Asamizu
  The First Laboratory for Plant Gene Research
  Kazusa DNA Research Institute
  Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
  Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
  Location/Qualifiers
    1..62
      /organism="Lotus corniculatus var. japonicus"
      /mol_type="mRNA"
      /isolate="Miyakojima MG-20"
      /db_xref="taxon:34305"
      /clone="MR054b08_f"
      /tissue type="roots"
      /clone_lib="Lotus japonicus roots"

ORIGIN
  Query Match      68.9%; Score 12.4; DB 3; Length 62;
  Best Local Similarity 92.9%; Pred. No. 1.6e+05;
  Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCACCTTATCTGGAT 16
   ||||| |||||
Db 39 TCACCTTCTGGAT 52

RESULT 19
AV963593 74 bp mRNA linear EST 14-MAR-2002
LOCUS

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DEFINITION AV963593 Nori Satoh unpublished cDNA library, egg Ciona
intestinalis cDNA clone cieg24107 5', mRNA sequence.
ACCESSION AV963593
VERSION AV963593.1 GI:19451892
SOURCE EST.
ORGANISM Ciona intestinalis
Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
REFERENCE Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
AUTHORS 1 (bases 1 to 74)
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@acidian.zool.kyoto-u.ac.jp.

FEATURES
    source
        1..74
            /organism="Ciona intestinalis"
            /mol_type="mRNA"
            /db_xref="taxon:7719"
            /clone="cieg24107"
            /tissue_type="whole animal"
            /dev_stage="egg"
            /clone_lib="Nori Satoh unpublished cDNA library, egg"

ORIGIN
Query Match 68.9%; Score 12.4; DB 1; Length 74;
Best Local Similarity 92.9%; Pred. No. 1.6e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ACTTATCTGGATT 18
    |||||
Db 18 ATTATCTGGATT 31

RESULT 20
TA92F10Q
LOCUS TA92F10Q 42 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 92f10, reverse sequence,
genomic survey sequence.
ACCESSION AL462451
VERSION AL462451.1 GI:11862749
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma
1 (bases 1 to 42)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajadream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
Project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nhlayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
    source
        1..42
            /organism="Trypanosoma brucei"
            /mol_type="genomic DNA"
            /strain="TREU927"
            /db_xref="taxon:5691"
            /clone="92f10"

ORIGIN
Query Match 67.8%; Score 12.2; DB 1; Length 42;
Best Local Similarity 82.4%; Pred. No. 1.9e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGTCACTTATCTGGATT 17
    |||||
Db 5 TGCCCTTATCTGGCTT 21

RESULT 21
AI308308/c
LOCUS AI308308 50 bp mRNA linear EST 10-DEC-1998
DEFINITION ta90f01.x1 NCI CGAP Brn20 Homo sapiens cDNA clone IMAGE:2051353 3',
similar to gb:M54927 MYELIN PROTEOLIPID PROTEIN (HUMAN);, mRNA
sequence.
ACCESSION AI308308
VERSION AI308308.1 GI:4002943
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Robert Jenkins, M.D., Mark Israel, M.D., Jim
Jacobson, Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES
    source
        1..50
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:2051353"
            /tissue_type="oligodendrogloma"
            /dev_stage="adult"
            /lab_host="DH10B"
            /clone_lib="NCI CGAP Brn20"
            /note="Organ: brain; Vector: pAMP1; mRNA made from
oligodendrogloma tissue, cDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."

ORIGIN
Query Match 67.8%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 2e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 TGTCATTATCTGGATT 17
    ||||| ||||| |||||
Db 37 TGTCATTATCTGGATT 21

RESULT 22
AQ073921/c
LOCUS
DEFINITION
  EP(3)3330 Drosophila melanogaster EP line Drosophila melanogaster
  genomic sequence recovered from Both 5' and 3' ends of P element,
  genomic survey sequence.
ACCESSION
  AQ073921
VERSION
  AQ073921.1 GI:3403963
KEYWORDS
  GSS.
SOURCE
  ORGANISM
    Drosophila melanogaster (fruit fly)
    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
    Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
    Ephydroidea; Drosophilidae; Drosophila.
  1 (bases 1 to 54)
  Liao, G.-C., Rehm, E.J. and Rubin, G.M.
  Insertion site preferences of the P transposable element in
  Drosophila melanogaster
  Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)
  10716700
  Contact: Gerald Rubin
  Berkeley Drosophila Genome Project
  University of California, Berkeley
  LSA Building, Berkeley, CA 94720-3200, USA
  Fax: 5106439947
  Email: Gerry@fruitfly.berkeley.edu
  Sequence recovery method was inverse PCR.

  Sequence orientation is forward strand relative to 5' end of P
  element

  The P element insertion position is base 19 in the 54 bases. This
  insertion position refers to the first base of the 8 base target
  recognition sequence.
  Class: transposon-tagged.
  Location/Qualifiers
    1..54
      /organism="Drosophila melanogaster"
      /mol_type="genomic DNA"
      /db_xref="taxon:7227"
      /clone_lib="Drosophila melanogaster EP line"
      /notes="Inverse PCR was performed on Drosophila
      melanogaster strains each of which contains a single EP
      transposable element insertion. (The generation of these
      insertion strains is described in Rorth P, Szabo K, Bailey
      A, Lavery T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes
      V, Ansorge W, Cohen SM. 1998. Systematic gain-of-function
      genetics in Drosophila. Development 6:1049-1057.) The
      resultant fragment for each strain was directly sequenced
      to determine the genomic sequence at the site of
      insertion. Details of the protocols used can be found at
      http://fruitfly.berkeley.edu/p_disrupt/inverse_pcr.html."

ORIGIN
  Query Match 67.8%; Score 12.2; DB 9; Length 54;
  Best Local Similarity 82.4%; Pred. No. 2e+05;
  Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  Qy 2 GTCACTTATCTGGATT 18
    ||||| ||||| |||||
  Db 22 GACACTTTCTGGCTTT 6

RESULT 23
AZ469856
LOCUS
DEFINITION
  1M0283B08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0283B08 R, genomic survey sequence.

ACCESSION
  AZ469856
VERSION
  AZ469856.1 GI:10627981
KEYWORDS
  GSS.
SOURCE
  ORGANISM
    Mus musculus (house mouse)
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  1 (bases 1 to 56)
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
  Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
  Niederhausern, A. and Wright, D. Weis, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0283 row: B column: 08
  Seq primer: CACACAGGAACACGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 56.
  Location/Qualifiers
    1..56
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0283B08"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /notes="Vector: PWD42nv; Purified genomic DNA from M.
      musculus C57BL/6J (male) was obtained from the Jackson
      Laboratory Mouse DNA Resource
      (http://www.jax.org/resources/documents/dnares/). The DNA
      was hydrodynamically sheared by repeated passage through a
      0.005 inch orifice at constant velocity. The sheared DNA
      was blunt end-repaired with T4 DNA polymerase and T4
      polynucleotide kinase. Adaptor oligonucleotides were
      ligated to the blunt ends in high molar excess. The
      adaptor DNA was purified and size-selected for a 9.5 to
      10.5 kb range using preparative agarose gel
      electrophoresis. Vector DNA was prepared from a derivative
      of pMD42 (GI4732114|gb|AF129072.1), a copy-number
      inducible derivative of plasmid R1. The vector was ligated
      with adaptors complementary to the insert adaptors and
      purified. The sheared, adaptor mouse DNA was annealed to
      adaptor vector DNA, and transformed into
      chemically-competent E. coli XL10-Gold (Stratagene) cells
      and selected for ampicillin resistance."

ORIGIN
  Query Match 67.8%; Score 12.2; DB 9; Length 56;
  Best Local Similarity 82.4%; Pred. No. 2e+05;
  Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  Qy 2 GTCACTTATCTGGATT 18
    ||||| ||||| |||||
  Db 1 GGCACCTGCTCGATT 17

RESULT 24
CR061632/c
LOCUS
DEFINITION
  Reverse strand read from insert in 3'HPRT insertion targeting and

```


chromosome engineering clone MHPPI28g02, genomic survey sequence.
 CR061632 1 GI:49795104
 GSS: genome survey sequence; MICR.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 59)
 Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
 Rogers,J. and Bradley,A.
 Direct Submission
 Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. <http://www.sanger.ac.uk/MICR>
 FEATURES
 source 1..59
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHPPI28g02"
 /clone_lib="MHPP"

Db 20 TGTCACCTTCACTGGAAT 36

Search completed: March 3, 2006, 11:01:40
 Job time : 989.737 secs

Query Match 67.8%; Score 12.2; DB 11; Length 59;
 Best Local Similarity 82.4%; Pred. No. 2e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GTCACTTATCTGGATT 18
 |||||
 Db 49 GTCCCTATCAGGATT 33

ORIGIN

RESULT 25
 CD940007
 LOCUS CD940007 60 bp mRNA linear EST 15-JUL-2003
 DEFINITION RAA_94 GenTag1 Zea mays cDNA, mRNA sequence.
 ACCESSION CD940007
 VERSION CD940007.1 GI:32787515
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 60)
 Genoplante.
 Genoplante, a major partnership french program in plant genomics
 Unpublished (2003)
 Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>
 and <http://genoplante-info.infobiogen.fr>).
 FEATURES
 source 1..60
 Location/Qualifiers
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="mixture"
 /db_xref="taxon:4577"
 /clone_lib="GenTag1"

Query Match 67.8%; Score 12.2; DB 6; Length 60;
 Best Local Similarity 82.4%; Pred. No. 2e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGTCACCTTATCTGGATT 17
 |||||

ORIGIN

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